#### STIC-Biotech/ChemLib

From: Sent:

Scheiner, Laurie Tuesday, September 09, 2003 8:38 PM STIC-Biotech/ChemLib

To: Subject: seq. search request

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SEP 10 2693

Please search SEQ ID NO:1 of application S.N. 09/849,729. Please also search antisense, if possible. Thanks: (STIC)

Laurie Scheiner Art Unit 1648 CM1 8E05 308-1122 8E12

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             4 (SENTINEL VIRUS)
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     ANSWER 1 OF 4 USPATFULL on STN
L3
AN
       2003:237383 USPATFULL
TΙ
       Sentinel virus II
TN
       Liu, Jen-Kuei, Palo Alto, CA, UNITED STATES
       Lewis, Samantha, San Francisco, CA, UNITED STATES
       Batz, Hans-Georg, Tutzing, GERMANY, FEDERAL REPUBLIC OF
       Ramaswamy, Latha, San Jose, CA, UNITED STATES
       Bohenzky, Roy, Mountain View, CA, UNITED STATES
       Lin, Yu-Huei, Sunnyvale, CA, UNITED STATES
       Montiel, Janine, Fremont, CA, UNITED STATES
       Chen, Benjamin P., Fremont, CA, UNITED STATES
PΙ
       US 2003165540
                          Α1
                               20030904
ΑI
       US 2001-849729
                          Α1
                               20010504 (9)
PRAI
       US 2000-202271P
                           20000505 (60)
       Utility
DT
FS
       APPLICATION
       Kenneth J. Waite, Roche Diagnostics Corporation, 9115 Haque Road, Bldg.
LREP
       D, P.O. Box 50457, Indianapolis, IN, 46250-0457
CLMN
       Number of Claims: 13
       Exemplary Claim: 1
ECL
DRWN
       1 Drawing Page(s)
LN.CNT 1307
AB
       The invention relates to a new virus, designated H101.c33 or
       Sentinel Virus II (SVII). Isolated SVII viruses,
       polynucleotides and proteins from SVII viruses, and antibodies which
       bind SVII virus and SVII viral proteins are provided. The
       polynucleotides, proteins, and antibodies of the invention may be used
       to detect SVII virus or infection by SVII virus in a susceptible
       individual. Additionally, polynucleotides of the invention may be
       inserted into recombinant expression vectors for recombinant production
       of viral proteins.
     ANSWER 2 OF 4 USPATFULL on STN
L3
AN
       2001:188386 USPATFULL
ΤI
       Hepatitis virus sentinel virus I (SVI)
IN
       Liu, Jen-Kuei, Palo Alto, CA, United States
       Bohenzky, Roy A., Mountain View, CA, United States
       Lin, Yu-Huei, Sunnyvale, CA, United States
       Chen, Benjamin P., Fremont, CA, United States
PΙ
       US 2001034018
                          Α1
                               20011025
       US 2000-732665
AΙ
                          Α1
                               20001208 (9)
PRAI
       US 1999-172696P
                           19991210 (60)
       Utility
DT
FS
       APPLICATION
       Kenneth J. Waite, Roche Diagnostics Corporation, 9115 Hague Road, Bldg.
LREP
       D, P.O. Box 50457, Indianapolis, IN, 46250-0457
CLMN
       Number of Claims: 18
ECL
       Exemplary Claim: 1
DRWN
       3 Drawing Page(s)
LN.CNT 1382
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB
       The invention relates to a new group of viruses, designated SVI.
       Isolated SVI viruses, polynucleotides and proteins from SVI viruses, and
       antibodies which bind SVI virus and SVI viral proteins are provided. The
       polynucleotides, proteins, and antibodies of the invention may be used
       to detect SVI virus or infection by SVI virus in a susceptible
       individual. Additionally, polynucleotides of the invention may be
       inserted into recombinant expression vectors recombinant production of
       viral proteins.
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ANSWER 3 OF 4 WPIDS COPYRIGHT 2003 THOMSON DERWENT on STN
AN
     2002-062234 [08]
                        WPIDS
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    C2002-017791
TI
     A new virus associated with cryptogenic non-A/non-G hepatitis, designated
     Sentinel Virus II is useful to detect and treat
     Sentinel Virus II infection.
DC
     B04 D16
     BATZ, H; BOHENZKY, R; CHEN, B; LEWIS, S; LIN, Y; LIU, J; MONTIEL, J;
TN
     RAMASWAMY, L; CHEN, B P
PΑ
     (LIUJ-I) LIU J; (HOFF) HOFFMANN LA ROCHE & CO AG F; (HOFF) ROCHE
     DIAGNOSTICS GMBH; (BATZ-I) BATZ H; (BOHE-I) BOHENZKY R; (CHEN-I) CHEN B P;
     (LEWI-I) LEWIS S; (LINY-I) LIN Y; (MONT-I) MONTIEL J; (RAMA-I) RAMASWAMY L
CYC
    96
PΙ
     WO 2001085770 A2 20011115 (200208) * EN
                                              20p
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            NL OA PT SD SE SL SZ TR TZ UG ZW
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            LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD
            SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW
     AU 2001065924 A 20011120 (200219)
     EP 1282692
                   A2 20030212 (200312)
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         R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT
            RO SE SI TR
     BR 2001010576 A 20030401 (200327)
     KR 2003032947 A 20030426 (200354)
     CZ 2002003631 A3 20030716 (200355)
     US 2003165540 A1 20030904 (200359)
ADT WO 2001085770 A2 WO 2001-EP5029 20010504; AU 2001065924 A AU 2001-65924
     20010504; EP 1282692 A2 EP 2001-943319 20010504, WO 2001-EP5029 20010504;
     BR 2001010576 A BR 2001-10576 20010504, WO 2001-EP5029 20010504; KR
     2003032947 A KR 2002-714822 20021105; CZ 2002003631 A3 WO 2001-EP5029
     20010504, CZ 2002-3631 20010504; US 2003165540 A1 Provisional US
     2000-202271P 20000505, US 2001-849729 20010504
FDT AU 2001065924 A Based on WO 2001085770; EP 1282692 A2 Based on WO
     2001085770; BR 2001010576 A Based on WO 2001085770; CZ 2002003631 A3 Based
     on WO 2001085770
PRAI US 2000-202271P 20000505; US 2001-849729
                                                 20010504
     WO 200185770 A UPAB: 20020204
     NOVELTY - A composition comprising isolated Sentinel
     Virus II (SVII) virus, is new.
          DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the
     following:
          (1) an isolated polynucleotide which is the sequence fully defined in
     the specification or its complement;
          (2) an isolated polynucleotide which hybridizes with the above
     sequence;
          (3) an isolated polynucleotide which encodes an SVII protein or its
     fragment;
          (4) an isolated polynucleotide whose complement encodes an SVII
     protein or its fragment, particularly an antisense polynucleotide;
          (5) a composition, particularly a vaccine composition, comprising an
     isolated SVII protein or its fragment;
          (6) an expression vector comprising an isolated polynucleotide
     transcription of which produces an SVII antisense polynucleotide;
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(8) a monoclonal antibody which binds as SVII virus or its protein; (9) detecting SVII virus, comprising contacting a sample with the above antibody and detecting antibody:protein complexes;

(7) an isolated polyclonal antisera which specifically binds an SVII

(10) detecting SVII virus, comprising contacting a sample with a probe which selectively hybridizes with an SVII polynucleotide and detecting hybridization.

virus or its protein;

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ACTIVITY - Anti-viral. No relevant biological data was provided. MECHANISM OF ACTION - None given. USE - The invention is used to detect and treat SVII infection. Dwq.0/1 ANSWER 4 OF 4 WPIDS COPYRIGHT 2003 THOMSON DERWENT on STN 2001-381643 [40] WPIDS C2001-116931 Novel virus, designated sentinel virus I, associated with cryptogenic, nonA-G hepatitis, and polynucleotides and polypeptides of virus useful for detecting SVI virus and/or SVI virus infection. B04 D16 BOHENZKY, R A; CHEN, B P; LIN, Y; LIU, J (HOFF) ROCHE DIAGNOSTICS GMBH; (BOHE-I) BOHENZKY R A; (CHEN-I) CHEN B P; (LINY-I) LIN Y; (LIUJ-I) LIU J WO 2001042299 A2 20010614 (200140)\* EN 62p RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW AU 2001022129 A 20010618 (200161) US 2001034018 A1 20011025 (200170) BR 2000016289 A 20020813 (200262) EP 1240189 A2 20020918 (200269) ENR: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR KR 2002065559 A 20020813 (200309) JP 2003516136 W 20030513 (200334) 81p CZ 2002001962 A3 20030716 (200355) ADT WO 2001042299 A2 WO 2000-IB2011 20001208; AU 2001022129 A AU 2001-22129

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20001208; US 2001034018 A1 Provisional US 1999-172696P 19991210, US 2000-732665 20001208; BR 2000016289 A BR 2000-16289 20001208, WO 2000-IB2011 20001208; EP 1240189 A2 EP 2000-985731 20001208, WO 2000-IB2011.20001208; KR 2002065559 A KR 2002-707427 20020610; JP 2003516136 W WO 2000-IB2011 20001208, JP 2001-543596 20001208; CZ 2002001962 A3 WO 2000-IB2011 20001208, CZ 2002-1962 20001208

FDT AU 2001022129 A Based on WO 2001042299; BR 2000016289 A Based on WO 2001042299; EP 1240189 A2 Based on WO 2001042299; JP 2003516136 W Based on WO 2001042299; CZ 2002001962 A3 Based on WO 2001042299

PRAI US 1999-172696P 19991210; US 2000-732665 20001208

WO 200142299 A UPAB: 20021007

NOVELTY - A composition (I), comprising isolated sentinel virus I (SVI) virus, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

- (1) an isolated polynucleotide (II) which:
- (a) selectively hybridizes with a 3847, 3844, 2499, 2499 or 2496 nucleotide SVI sequence (S1-S5), all fully defined in the specification;
  - (b) is complementary to (a);
  - (c) encodes an isolated SVI protein or its fragment; or
- (d) is complementary to an isolated polynucleotide encoding an isolated SVI protein or its fragment, the nucleotide sequence of (II) is distinct from the genomic sequences of TTV strains SANBAN and TUS01;
- (2) a composition comprising an isolated SVI protein or its fragment (III) which is serologically distinct from proteins of TTV strains SANBAN and TIS01;
  - (3) a vaccine composition comprising (III) and an excipient;
- (4) an expression vector comprising an isolated polynucleotide encoding an SVI protein or its fragment which is serologically distinct from proteins of TTV strains SANBAN and TUS01;
  - (5) an expression vector comprising an isolated polynucleotide, where

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transcription of the isolated polynucleotide results in the production of an SVI antisense polynucleotide which is not an antisense polynucleotide that forms a duplex with an RNA transcript from TTV strains SANBAN and TUS01;

- (6) an isolated polyclonal or monoclonal antibody (IV) which binds (III); and
- (7) an antibody (V) that binds to an SVI virus whose genome contains (S1-S5).

ACTIVITY - Antiviral.

No biological data is given.

MECHANISM OF ACTION - Vaccine; antisense gene therapy.

USE - (II), (IV), (V) are useful for detecting SVI virus. The method involves contacting a sample with:

- (a) (IV) which binds (III) but does not bind TTV strains SANBAN and TUS01 or its proteins, and detecting (IV)-(I) complex; or
  - (b) (II) which selectively hybridizes to:
- (i) a SVI polynucleotide but does not selectively hybridize with polynucleotides of TTV strains SANBAN and TUS01; or
- (ii) a target polynucleotide of a viral genome which comprises(S1-S5), and detecting SVI virus by detecting hybridization of (II)-SVI polynucleotide or detecting hybridization of the probe with the target, respectively; or
- (iii) the SVI virus and detecting SVI virus by detecting SVI virus-(V) complexes.
- (All claimed). Probes and primers derived from SVI polynucleotide sequences which comprise a sequence of (S1)-(S5) is useful for identifying and isolating new variants of SVI. SVI polynucleotides are useful for detecting SVI virus, producing SVI polypeptides, constructing SVI-based expression/transduction vectors and as antisense oligonucleotides or for construction of antisense SVI vectors. Antisense SVI polynucleotides block expression of SVI proteins and/or SVI viral replication in SVI infected cells, and thus are useful for treating SVI infections. SVI polypeptides are useful in vaccines for preventing SVI infection and for treating SVI infection. (IV) or (V) is useful for detecting and/or identifying SVI virus and may also be useful for isolating viral particles and/or viral proteins.

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### SUMMARIES

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			Montiel, J., Batz, H.G. and Chen, B.	
7, L.,	Ramaswamy	in, Y.H.,	Liu,J.K., Lewis,S., Bohenzky,R., Lin,Y.H., Ramaswamy,L.,	AUTHORS
			<b>L</b>	EFERENCE
			Viruses; unclassified viruses.	
			Sentinel virus II	ORGANISM
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Best Local Similarity
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                                                                                                                                                                                                                                                            ORGANISM
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                                                                    369;
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   13
                                                                                                                                                                                                                                                                                                    372 bp
Sequence 2 from Patent WOO185770.
                                              ы
                                                                                                                                                                    Patent: WO 0185770-A 2 15-NOV-2001;
Location/Qualifiers
1. 372
                                                                                                                                                                                                    Montiel, J., Batz, H.G. and Sentinel virus II
                                                                                                                                                                                                                                                           Sentinel virus II
Sentinel virus II
                                                                                                                                                                                                                                                                                             AX301835.1
                                                                                                                                                                                                                           Liu, J.K., Lewis, S.,
                                                                                                                                                                                                                                                  Viruses;
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                                              GATCMGGAAACGYTTSGCTCGGTGCATGCAGAAGGACGGGWTGAAGGCGGACGGGATTGA
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                                                                    Conservative
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                                                                                                                                                                                                                                                  unclassified viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                         /organism="Sentinel virus II"
/mol_type="genomic DNA"
/db_xref="taxon:179884"
109 c 107 g 71 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Sentinel virus"
                                                                                                                                                                                                                                                                                              GI:17382896
                                                                               98.8%;
99.5%;
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                                                                                                                                                                                                                 Bohenzky,R.,
G. and Chen,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 369; DB 6;
Pred. No. 1.2e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 g
                                                                   Score 366.6; DB 6;
Pred. No. 3.5e-60;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79
                                                                                                                                                                                                                             Lin, Y.H., Ramaswamy, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 371
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                                                                                          Length 372;
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AC127800/c
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Muzny, D. Maria, Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Badechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Balawin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Balawin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Baiswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bristalo, K., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chu, J., Chao, Y., Chan, Y., Chen, Y., Chen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC127800.3 GI:25078136
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le CH230-30C5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12
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On Nov 19, 2002 this sequence version replaced gi:23194910.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Tingya, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consists entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 232092) Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Rives, C., Rodkey, G., Scherer, S., Scott, G., Shatsman, S., Shen, Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
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                                                                                                                                                                                                        NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently

consists of 2 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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                                                                                                                                               230152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: BCM
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                                                                                                             230252
1. .232092
/organism="Rattus norvegicus"
                                                                Location/Qualifiers
                                                                                                      230151: contig of 230151 bp in length 230251: gap of unknown length 232092: contig of 1841 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 CGTCTACGCG
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Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, B., Bade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED RATTUS norvegicus (Norway rat)
Rattus norvegicus
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Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L. Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., R
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/db_xref="taxon:10116"
/clone="CH230-30C5"
40897 c 41228 g 691
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Pred. No. 2
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The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                  250765
250865
256280
256380
257689
257789
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Center clone name: CH230-unknown
Center clone name: CH230-unknown
Center clone name: CH230-unknown
Center Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 219057 bases at least Q40
Consensus quality: 227727 bases at least Q30
Consensus quality: 227727 bases at least Q20
Estimated insert size: 232446; sum-of-contigs estimation
Estimated insert size: 23246; sum-of-contigs
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Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
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                           /mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-unknown"
                                                                                                                                                                                           1. .259427
                                                                                                                                               /organism="Rattus norvegicus"
                                                                                                                                                                                                                              Location/
                                                                                                                                                                                                                                                  250764: contig of 250764 bp in length 250864: gap of unknown length 250279: contig of 5415 bp in length 250379: gap of unknown length 257688: contig of 1309 bp in length 257788: gap of unknown length 257789: contig of 1639 bp in length.
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RESULT 5
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Barbaria, J., Benton, J., Bimage, R., Blankenburg, K., Bonnin, D., Buuck, J., Benton, J., Bimage, R., Blankenburg, K., Bonnin, D., Bunck, J., Brown, M., Brown, M., Bryant, N.P., Buuck, J., Burch, P., Burkett, C., Burrell, K.L., Brown, M., Bryant, N.P., Bunck, J., Charcon, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davild, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Davild, M.L., Davis, C., Davy-Carroll, D., Dederich, D.A., Davild, M.L., Davis, C., Davy-Carroll, D., Dederich, D.A., Davild, M.L., Davis, C., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Davild, M., Galle, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Garza, N., Gill, R., Gourell, J.H., Guevara, M., Gannaratne, P., Hale, S., Hamilton, K., Earnhart, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, W., Louiseged, H., Lozdo, R., Lucier, A., Lucier, R., Luna, R., Ma, J., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Lichtarge, C., Lieu, C., Liu, J., Liu, W., Louiseged, H., Manses, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Martin, R., Martin, R., Martindale, A., Martinez, E., Massey, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Martin, R., Martindale, A., Martinez, E., Miner, S., Morgan, M., Nowleyen, A., Nguyen, N., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Sudety, G., Shen, H., Shooshtari, N., Sisson, I., Sudety, G., Shen, H., Shooshtari, N., Sisson, I., Sudety, G., Shen, H., Stone, H., Stone,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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MTG- HTGS PHASE1; HTGS_DRAFT; HTGS_ENRICHED
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142765. .145383
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a 41912 c 41400 g
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Pred. No. 2
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Tamerisa, K., Tang, H.,

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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL Submitted (23-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 23, 2002 this sequence version replaced gi:23322531. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
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Direct Submission
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Baylor Plaza, Houston,
3 (bases 1 to 284938)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This sequence may represent more than one clone. NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
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Consensus quality: 270163 bases at least Q40
Consensus quality: 273610 bases at least Q30
Consensus quality: 275512 bases at least Q30
Consensus quality: 275512 bases at least Q20
Estimated insert size: 275684; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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258110
2581396
261496
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275502
278036
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274208
274308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Baylor College of Medicine
Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.hgsc.bcm.tmc.edu/
258009: contig of 258009 bp in length
258109: gap of unknown length
261395: contig of 3286 bp in length
261495: gap of unknown length
272813: contig of 11318 bp in length
272913: gap of unknown length
272913: gap of unknown length
274207: contig of 1294 bp in length
274307: gap of unknown length
275401: contig of 1094 bp in length
275401: contig of 1094 bp in length
27501: gap of unknown length
27501: gap of unknown length
278035: contig of 2534 bp in length
279756: contig of 1621 bp in length
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COMMENT

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                                                                                                                                                                                                                 1 (bases 1 to 1926)
Horlick,R.A. and Chelsky,D.
Method for maintenance and selection of episomes
Patent: US 6417002-A 4 09-JUL-2002;
                                                                                                                                                                                                                                                                                 Unknown
                                                                                                                                                                                                                                                                                                                                    Sequence 4 from patent US 6417002. AR217867
                                                                                                                                                                                                                                                                                              Unknown.
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                                                                                                                                                                                                                                                                      Unclassified.
                                                                                                              Similarity
              GACCGCYGACGTCCTTGGCGGGGGGAGCGAGGACCGAGAACCAAGACGACGAGGACGAGGACGT 150
GAAGGACGGGWTGAAGGCGGACGGGATTGACGACGACGACGACGATTGCGATGAAAGATGG 90
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872 c 352 g
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1149. .4548
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261496. .263006
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266927. .268487
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258110. .259135
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4599. .6337
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mol_type="genomic DNA"
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281224: contig of 1368 bp in
281324: gap of unknown length
281328: contig of 3614 bp in
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Pred. No. 6.8;
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Pred. No. 2.6;
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                                                                     Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N. Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Reddix-Dugue, N., Schueler, M.G., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L., Wetherby, K.D., Miggins, L., Young, A., Zhang, L.-H. and Green, E.D.
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AC115529.2
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               Green, E.D
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135924 bp
Rattus norvegicus clone RP31-42022
DRAFT SEQUENCE, 9 ordered pieces.
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Sequence 2 from patent US 5976807.
AR083152
                                               Unpublished
                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                            Rattus norvegicus
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Rattus norvegicus (Norway rat)
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Horlick,R.A., Damaj,B.B. and Robbins,A.K.
Eukaryotic cells stably expressing genes
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                    Submitted (30-AUG-2002) NIH Intramural Sequencing Grovemont Circle, Gaithersburg, MD 20877, USA On Aug 30, 2002 this sequence version replaced gi
                                                                                                                                                                                                                                                                  Green, E.D
                                                                                                                                                                                                                                                                                                         Grovemont
                                                                                                                                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                    (bases 1 to 135924)
Center project name: cxm
Center clone name: 042022
                                                             Contact: nisc_zoo@nhgri.nih.gov
                                                                                                           Center: NIH Intramural Center code: NISC
                                                                                  Web site: http://www.nisc.nih.gov
                                         ----- Project Information
                                                                                                                                                      ----- Genome Center
                                                                                                                                                                                                                                                                                                         (20-MAR-2002) NIH Intramural Sequencing Center, 8717 Circle, Gaithersburg, MD 20877, USA
                                                                                                                           Sequencing Center
                                                                                                                                                                         gi:19551131
                                                                                                                                                                                                                    Center,
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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least BX average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a phase death of the phase of the low-quality ends of sequence. with a Phrap-derived quality score. indicated

Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 134458 bases at least Q40
Consensus quality: 134732 bases at least Q30
Consensus quality: 135037 bases at least Q20
Insert size: 134000; agarose-fp
Insert size: 134124; sum-of-contigs
Quality coverage: 9.87x in Q20 bases; agarose-fp
Quality coverage: 9.87x in Q20 bases; sum-of-contigs

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source
                                                                                                                                                                                                      the accession number will be preserved.

1 10522: contig of 10522 bp in length
10523 10622: gap of unknown length
10623 40668: contig of 30046 bp in length
40669 40768: gap of unknown length
70574 70673: gap of unknown length
70574 774331: contig of 3660 bp in length
70574 74331: contig of 3660 bp in length
70574 74332: gap of unknown length
70574 74333: contig of 3660 bp in length
70574 7676: contig of 6226 bp in length
70574 7676: contig of 6226 bp in length
70574 711549: contig of 6226 bp in length
70574 711549: contig of 6226 bp in length
70574 711549: contig of 6226 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and by the finished sequence as soon as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                           111550
111650
113765
                                                                                                 113865
organism="Rattus norvegicus"
                                                             Location/Qualifiers
                                                                                                                                                                                         111649:
                                                                                                                        gap of unknown length
contig of 2115 bp in
gap of unknown length
                                                                                          contig of 22060
                                                                                       ij
                                                                                                                                                  length
                                                                                       length
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FEATURES

/mol\_type="genomic DNA" /strain="Brown Norway"

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AUTHORS
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AC135485/c
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Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalbbechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
                                                                                                                                                                                                                                                                                                                             HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                 236021 bp DNA linear HTG 20-NOV-2002 Rattus norvegicus clone CH230-22003, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                        Rattus.
                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                              AC135485.2 GI:25139082
                                                                                                                                                                                                                                                                                                                                                                                                                   AC135485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGACGAGGACGAGGACGAGGACAAGGA 87472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCAGAAGGACGGGWTGAAGGCGGACGGGATTGACGACGACGACGACATTGCGATGAAAGA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33598
                                                                                                                                                                                                                                                   (bases 1 to 236021)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      unordered pieces.
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85257. .111549
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113865. .135924
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111650. .113764
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/clone_lib="RP31"
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3 c 32360 g
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                                                                                                                                                                                                                                                                                         Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 49.6;
Pred. No. 5.
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                                                                                                                                                                  Barnstead, M., Benahmed, F.,
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TITLE JOURNAL REFERENCE

AUTHORS TITLE JOURNAL

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu

Project Information

Center: Baylor Co

College of Medicine

Center project name: KBVL Center clone name: CH230-22003

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Bgan, A., Bacotto, M., Bugene, C., Evans, C.A., Falls, T., Fanl, G., Ferrandez, S., Finley, M., Flaggy, N., Forbes, L., Foster, M., Gostea, M., Gabisi, A., Ganta, R., Garcia, A., Garrar, M., Glevara, M., Gabres, C.M., Gabisi, A., Ganta, R., Garcia, A., Garrar, T., Garca, M., Garrar, M., Glevara, M., Gharrar, T., Garcia, A., Garrar, M., Glevara, M., Gharrar, M., Glevara, M., Gharrar, M., Glevara, M., Gharrar, M., Garrar, M., Glevara, M., Gharrar, M., Garcia, A., Garcia, A., Garcia, A., Garrar, M., Garcia, M., Handlison, M., Hamilton, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Harrandez, J., Hadiline, B., Holline, B., Hohelos, B., Johnson, R., Johnson, A., Hogues, M., Backson, A., Johnson, B., Johnson, R., Johnson, R., Johnson, B., Johns
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Assembly program: Phrap;

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RESULT 10
AC098552
                                                                                                                                                                             KEYWORDS
SOURCE
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Best Local (
                                             AUTHORS
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AC098552.6 GI:30521633
HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                    2/0301 DP DNA linear HTG 10-MAY-2003 Rattus norvegicus clone CH230-75020, *** SEQUENCING IN PROGRESS ***, 13 unordered pieces.
Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D. Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden,
                                                                                      Rattus.
                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                      Rattus norvegicus
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NOTE: This is a 'working_draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        ĆĠ 38335
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                                                               (bases 1 to 278501)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 132351: contig of 132351 bp in length
132352 132451: gap of unknown length
132452 236021: contig of 103570 bp in length
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6765. ..6944
/note="clone_boundary
clone_end:T7
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53354 c 49978 g 59441 t 13678 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-22003"
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clone_end:T7"
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                                                                                                           Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 49.6;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ed. No. 5.3;
Mismatches
                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45;
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                                         Adams, C., Alder, J.,
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Cardenas, V., Carter, K., Chen, G., Chen, R., Chen, J., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox.C., Coyle, M., Cree, A., D'Souza, L., Davis, C., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Delgado, O., Danson, S., Dermo, C., Dingy, Dinh, H., Divya, K., Dapper, H., Dugan-Rocha, S., Dunn, A., Dubhin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Bugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagy, M., Forbes, L., Poster, M., Garza, M., Gebregeorgia, B., Geer, K., Gill, R., Grady, M., Guerra, M., Guaratme, P., Haaland, M., Hamilton, C., Hamilton, K., Harvey, Y., Havulak, P., Hawes, A., Henderson, M., Hennandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Morris, K., Morris, S., Munidasa, M., Murphy, M., Naris, S., Mangum, S., Morris, S., Munidasa, M., Murphy, M., Naris, S., Parks, K., Pasternak, S., Pall, H., Perez, A., Perez, L., Fannkoch, C., Pasternak, S., Pall, H., Perez, A., Perez, K., Regier, M.A., Faigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Reigh, R., Reigh, R., Reigh, R., Shetter, S., Soott, G., Shatsman, S., Shen, H., Shetty, J., Shvarebeyn, A., Sisson, I., Sitter, C.D., Sman, S., Shen, H., Shetty, J., Shvarebeyn, A., Sisson, I., Shter, C.D., Sman, S., Shen, H., Shetty, J., Walter, F., Mang, J., W
Direct Submission

AL Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genotes, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 10, 2003 this sequence version replaced gi:23268777.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (24-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baldwin,D., Bandaranaike,D., Barber,M.,
Biswalo,K., Blair,J., Blankenburg,K., B
Bryant,N., Buhay,C., Burch,P., Burreill,
Cardenas,V., Carter,K., Cavazos,I., Cea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat Genome Sequencing Consortium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Worley, K.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 278501)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barnstead, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Benahmed, F.,
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BASE COUNT
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      Query Match
Best Local Similarity
                                                                                                                                misc_feature
                                                                                                                                                                            misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This sequence may represent more than one clone. NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
                                                                                              71844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270968
271068
272452
272552
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269776
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8650
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260576
262101
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Assembly program: Atlas 3.0;
Consensus quality: 250165 bases at least Q40
Consensus quality: 25562 bases at least Q30
Consensus quality: 256167 bases at least Q20
Estimated insert size: 251291; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: GHJP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         274193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Baylor Co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/
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                                                                                       /note="wgs contig"
259200. 260475
/note="wgs_contig"
a 60550 c 60353 g
                                                                                                                                                                            256383. .257710
/note="wgs_contig"
257761. .258974
                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                       /note="wgs_contig"
256383. .257710
                                                                                                                                                                                                                                                                  /note="wgs_contig"
8650. .10198
                                                                                                                                                                                                                                                                                                                                                                                             organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                          Location,
                                                                                                                                                                                                                                                                                                                                   clone="CH230-75020"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262100 contig of 1525 bp in length
262200 gap of unknown length
263833 contig of 1633 bp in length
263833 gap of unknown length
265076 contig of 1143 bp in length
265176 gap of unknown length
266562 contig of 1386 bp in length
266562 gap of unknown length
268410 contig of 1748 bp in length
268775 contig of 1748 bp in length
268710 gap of unknown length
268710 gap of unknown length
268715 gap of unknown length
270967 contig of 1265 bp in length
271067 gap of unknown length
271067 gap of unknown length
272451 contig of 1092 bp in length
272571 gap of unknown length
272451 contig of 1384 bp in length
272451 contig of 1541 bp in length
274192 gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8549: contig of 8549 bp in length
8649: gap of unknown length
260475: contig of 251826 bp in lengt
260575: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                            275796: contig of 1604
275896: gap of unknown
278501: contig of 2605
      13.4%;
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DB ...2;
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                          Length 278501;
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SOURCE
ORGANISM
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                                                                     Biswald, K., Blair, J., Burch, P., Burrell, K., Calderon, E., Eryant, N., Bhhay, C., Burch, P., Burrell, K., Calderon, E., Cardens, V., Carter, K., Cavazos, I., Cesar, H., Center, A., Chenco, J., Chacko, J., Chacko, J., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockreil, R., Cox, C., Coyle, M., Cree, A., Diouza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davila, M.L., Barotto, M., Eugene, C., Coyle, M., Cree, A., Dion, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Frases, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Guerra, W., Guerra, M., Hogues, M., Hollins, B., Houles, S., Kelly, S., Hume, J., Idlabird, D., Jackson, A., Hogues, M., Hogues, M., Mally, K., Kunz, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, J., Liu, J., Longacre, S., Lopez, J., Lorensulwa, J., Mallor, J., Mallo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101632 CG 101633
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Taylor,T., ....
Valas,R., Vera,V., V...
Valas,R., Wang,S., Warren,J.,
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7 unordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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On Sep 19, 2002 this sequence version replaced gi:21909215.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequening reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature table.
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                     /db_xref="taxon:10116"
/clone="CH230-18C5"
                                                        organism="Rattus norvegicus"

/mol_type="genomic DNA"
                                                                                                                 Socation/Qualifiers
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272170: contig of 1016 b
272270: gap of unknown 1
272270: gap of unknown 1
273543: contig of 1273 b
273543: gap of unknown 1
275350: contig of 1707 b
275450: gap of unknown 1
277162: contig of 1712 b
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271154:
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279148: contig of 1886
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                                                                                                                                                                                                                                                                                                                                    Unpublished
(Chases 1 to 152564)
(Chases 1 to 152564)
McPherson, J.D. and Waterston, R.H.
Direct Submission
Direct Submission
Submitted (17-JUL-2002) Genome Sequencing Center,
Submitted (17-JUL-2008) USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: M_BB0510G05
                                                                            Center: Washington University Genome Center code: WUGSC
                                                                                                                                                  Parkway, St. Louis, MO 63108,
On Feb 21, 2003 this sequence
                                                                                                                                                                                                         Parkway, St. Louis, MO 63108, USA 4 (bases 1 to 152564) McPherson, J.D. and Waterston, R.H. Direct Submission
                                                                                                                                                                                                                                                                                                 3 (bases 1 to 152564)
MCPherson, J.D. and Waterston, R.H.
Direct Submission
                                       Contact: submissions@watson.wustl.edu
                                                        Web site:http://
                                                                                                                                                                                       Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 152564)
McPherson,J.D. and Waterston,R.H.
The sequence of Mus musculus clone
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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complement(266213...26
/note="clone_boundary"
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                                                                                                                                                2003 this sequence version replaced gi:27734044.
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                                                      /genome.wustl.edu/gsc/index.shtml
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AC115847/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                   RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gape, D., Galagan, J., Gardyna, S., Ginde, S., Good, S., Goyette, M., Garden, L., Grand-Pierre, N., Ginde, S., Gord, S., Goyette, M., Garden, L., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Muneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., O'Iver, J., Peeterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Ries, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tooham, K., Travers, M., Travis, N., Tridilo, J., Vassilev, H., J., Tasis, N., Travis, N., Travis, N., Vassilev, H., J., Vassilev, H., J., Vassilev, H., J., Tasis, N., Travis, N., Travis, N., Tasis, N., Travis, N., Tr
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3 (bases 1 to 181931)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Birren,B., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
                                                                                                                                                                                                                                                Strauss, N., Subramanian, A., Talamas, J., Tesfa Topham, K., Travers, M., Travis, N., Trigilio, J. Viel, R., VO, A., Wilson, B., Wu, X., Wyman, D., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                                                                Submitted (22-MAR-2002) Whitehead Institute/MIT Ce Research, 320 Charles Street, Cambridge, MA 02141,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren,B., Linton,L., Nusbaum,C. and Lander,E. musculus, clone RP24-245J15
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
Mus musculus (house mouse)
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Mus musculus clone RP24-245J15,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="5"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                 Ye, W.J., Young, G.,
                                                                                                                                                                                                                                                                                                                                                         , Vassiliev, H.,
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11, USA
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Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., Fitzcerald, M., FitzHgh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Jamazares, R., Landers, T., Leboczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Muzphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Riebock, M., Riley, R., Riee, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Taveris, N., Trigilio, J., Vaussiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Viens, S., Shots sion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   consists of 24 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence, as soon as it is available and by the finished sequence, as soon as it is available.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center clone name: 245 J 15

Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of read Assembly program: Phrap; version 0.960731

Consensus quality: 175364 bases at least Q30

Consensus quality: 17921 bases at least Q30

Consensus quality: 178974 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality coverage: 7.8 in Q20 bases; Quality coverage: 7.7 in Q20 bases;
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Center clone name: 245_J_15
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Insert size: 179631; sum-of-contigs
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36779:
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of 653 bp in
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of 1243
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58745
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                /note="assembly_fragment"
                                                  /note="assembly_fragment"
58745. .61856
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54761. .58644
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45738. .47265
                                                                                                                                                                                           /note="assembly_fragment"
42141. .43329
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                                                                                                                                                                                                                                                                          38330
                                                                                                                                                                                                                                                                                                                                      36017
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                                                                                                                   /note≃"assembly_fragment"
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP24-245J15"
                                                                                                                                                                                                                                                                                                                                                             note="assembly_fragment
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58644: contig
58744: gap of
61856: contig
61956: gap of
65844: contig
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g of 3888 bp in length
of 100 bp
g of 3976 bp in length
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g of 2163 bp
f 100 bp
g of 2798 bp
g of 3884 bp
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of 3112 bp
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g of 2134 bp
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SOURCE
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AC098082/c
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MIZEL D. Martie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barastead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Benahmed, F., Eryant, N., Buhay, C., Burch, P., Burreil, K., Calderon, B., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Claveland, C., Cockreil, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Dayla, C., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Draper, H., Dugan, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Dayla, C., Davis, C., Davis, C., Davis, C., Davis, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Coyle, M., Cree, A., D'Souza, L., Coyle, M., Cree, A., D'Souza, L., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan, R., Cox, C., Coyle, M., Chen, Z., Chu, J., Fan, G., Farls, T., Fan, G., Farls, T., Fan, G., Farls, T., Fan, G., Farls, T., Fan, G., Farls, M., Guerra, M., Gebregorgis, B., Geer, K., Galli, R., Gardy, M., Guerra, M., Gebrey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hadun, S.L., Hodgson, A., Hogues, M., Guerra, W., Gebrey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, J., Jackson, L., Lubow, H., Ladun, S.L., Hodgson, A., Hogues, M., J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malioy, K., Mangum, A., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malioy, K., Mangum, A., Martinez, E., Mortis, S., Munidasa, M., Murphy, M., Nair, L., Luis, M., J., Lee, M., Mahindartne, M., Mahmoud, M., Pal, S., Marks, K., Marks, K., Mar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus clone CH230-129A9, ***, 3 unordered pieces.
AC0980B12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Norway rat)
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124208. .149441
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108536. .124107
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93902. .108435
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/note="assembly_fragment"
79706. .93801
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61.5%;
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; Pred. No. 11;
1; Mismatches
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Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pul, L. L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodeugren, E., Song, X. -Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldrov, A., Trejos, Z., Usmani, K., Wang, Q., Wang, S., Warren, J., Waldrov, L., Walker, B., Wang, J., Warght, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, J., Zhou, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Direct Suhmission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:22855414.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome specifications will be indicated in the feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          table.
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                                                                                                                                                                                                                                                 NOTE: Estimated insert size may differ from sequence length
(see http://www.hsgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 3 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
                                                                                                                                                                                      be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project Information
Center project name: GGFY
Center clone name: CH230-129A9
Consensus quality: 201734 bases at least Q40
Centersus quality: 201734 bases at least Q30
Centersus quality: 205336 bases at least Q20
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                   212206
212306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: hgsc-help@bcm.tmc.edu
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212205: contig of 212205 bp in length 212305: gap of unknown length 213509: contig of 1204 bp in length
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Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.
                                                                                  Submitted (15-JUN-2002) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC124637 236539 bp DNA linear HTG 06-MAR-2003 Mus musculus clone RP23-458B6, WORKING DRAFT SEQUENCE, 14 unordered
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Submitted (06-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 6, 2003 this sequence version replaced gi:28631255.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as soon as it is available be preserved.
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Insert size: 235239; sum-of-contigs
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Center clone name: 458_B_6
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Search completed: September 15, 2003, 00:00:30 Job time : 2091 secs

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Listing first 45 summaries
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1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
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AAQ36859
AAF76910
AAI72775
AAA30290
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                   Sentinel Virus II
Randomising oligon
PCR primer for 5'
Sequence containin
Oligo #7 for cloni
Kaposi's sarcoma-a
Nucleotide sequenc
                                                                                                                                                                                                                              Description
  Kaposi's sarcoma-a
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#### ALIGNMENTS

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RESULT 1
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ID AAI77
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XX Sent
XX SVII
XW VACC
XX Sent
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XX Sent
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XX IIII
XI COS
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                                                                                                    unsure
                                                                                                                                                                          Sentinel virus II.
                                                                                                                                                                                              SVII; H101.c33; hepatitis virus; infection; therapy; diagnosis; vaccine; ss.
                         /note= "encodes Met or complement (1..371) /*tag= d
                                                                                                  /partial
/note= "Xaa=unknown; ORF Pl, encodes AAM50524"
14..16
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/note= "encodes
41..43
/transl_except= "(pos:96..98,aa:Xaa)
/note= "Xaa=unknown; ORF M1, encodes AAM50525"
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Sentinel Virus II positive strand.

12-MAR-2002 (first entry)

AAI70920;

AAI70920 standard; DNA; 371 BP.

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found in serum samples from chronic hapatitis patients, particularly hepatitis C virus patients and patients superinfected with more than one type of hepatitis virus. The invention provides SVII viruses polynucleotides, proteins, and antibodies which bind SVII virus and viral proteins. These can be used to detect SVII virus or infection by SVII virus, and the polynucleotides can be inserted into recombinant expression vectors for production of viral proteins. Vaccines for prevention and/or treatment of SVII infection are also provided. These may be protein- or DNA-based vaccines.
                                                                                                                                                                                                                 that is associated with cryptogenic, non-A/non-G hepatitis. The prototypic virus comprises a DNA genome of at least 371 bases. DNA clones comprising the genomic DNA were isolated using a modification of the representation different analysis (RDA) method in which serum from a cryptogenic hepatitis patient was used as the source of tester DNA. 3 Putative open reading frames were identified, 1 on the positive strand (P1) of the genomic DNA and 2 on the negative strand (M1 and M2). Conceptual translations of these ORFs are given in AAM50524-26. SVII was found at a high prevalence in serum from acute hepatitis patients, and was also found in common acute hepatitis patients.
                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of the positive strand of a new hematitis virus, designated Sentinel virus II (SVII) or H101.c33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A new virus associated with cryptogenic non-A/non-G hepatitis, designated Sentinel Virus II is useful to detect and treat Sentinel Virus II infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 35; 20pp;
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Chen B;
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Best Local
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                                        New method of systematic polypeptide evolution by reverse translation - by linking each polypeptide in sample mixt. individualised mRNA allowing further synthesis of selected polypeptide(s)
                        Example; Page 55;
                                                                                      WPI; 1992-080018/10.
                                                                                                      Gold L,
                                                                                                                                           02-AUG-1990;
                                                                                                                                                            01-AUG-1991;
                                                                                                                                                                              20-FEB-1992.
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                                                                                                                                                                                                                 Synthetic
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                        102pp; English.
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Best Local
               SPERT is used to select novel polypeptides that bind the antibody of the epitope commonly recognised by the antisera from autoimmune mice which are the fl progeny of a cross of NZB and NZW parents (Portanova et al., J. Immunol. 144, 4633, 1990). The known epitope consists of ca. 10 amino acids at the N-terminus of the histone HZB protein. To make mRNA encoding candidate polypeptides a 5' fixed sequence composed of a T7 promoter sequence and a ribosome binding site which is recognised by both prokaryotic and eukaryotic ribosomes, terminating in a restriction endonuclease site is synthesised and colone terminating in a restriction endonuclease site is synthesised and colone terminating in a restriction endonuclease site is synthesised and colone terminating in a restriction endonuclease site is synthesised and colone terminating in a restriction endonuclease site is synthesised and colone terminating in a restriction endonuclease site is synthesised and colone terminating in a restriction endonuclease site is synthesised and colone terminating in a restriction endonuclease site is synthesised and colone terminating in a restriction endonuclease site is synthesised and colone terminating in a restriction endonuclease site is synthesised and colone terminating the synthesis of the synthesis and colone terminating in a restriction endonuclease site is synthesis and colone terminating the synthesis of the synthesis and colone terminating the synthesis and the synthesis 
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22-JUN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-1992;
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                                                                                                                                                                                                                                         Example 1; Page 84; 98pp; English
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RESULT 4
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ID AAF7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is placed into a restriction site to provide an mRNA encoding the C-terminal trailer sequence of ca. 100 nuclectides lacking stop codons In addition, a 3' primer annealing site is provided so that cDNA synthesis can be accomplished on the mRNA recovered from partitioned ribosome complexes. See also AAQ36845-63. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                  Gold
                                                                                                                                                                                                                                                                                                                                                                                                                           (TUER/)
(PRIB/)
(SMIT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ligand isolation;
SPERT; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF76910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JAN-1992;
02-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence containing a 120 repeat of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF76910;
                                                                                                                                                                                                                                                                                    Isolating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6194550-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78;
                                                                                                                                                                                                                                                                                                                                                                                                                           GOLD L.
TUERK C.
PRIBNOW
SMITH J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTGCATGCAGAAGGACGGGWTGAAGGCGGACGACGACGACGACGACGACGA
                                                                                                                                                                                                                                                                                                                                                                             Tuerk C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACGAGGACGTCTACG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACGACGACGACG 135
                                                                                                                                                                                                                                 a polypeptide ligand to a target molecule, useful for c assays, comprises partitioning candidate mixtures comprised me complexes or mRNA polypeptide copolymers relative to their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92US-0829461.
90US-0561968.
91US-0739055.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0197649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         systemic polypeptide evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
                                                                                                                                                                                                                                                                                                                                                                                  Pribnow
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                  Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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The present sequence was used in an example illustrating an invention relating to a method for isolating a polypeptide ligand for a desired target molecule. The method involves synthesising a nucleic acid mixture comprising mRNA having translatable and non-translatable regions and a mixture of nucleic acid.polypeptide coppolymers, each comprising the mRNA and a polypeptide encoded by its associated mRNA. The copolymers are

diagnostic assays, of ribosome comple: affinity to the ta:

complexes or the target mo

target molecule

Example;

Column

39; 35pp;

English.

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RRESULT 5
AAA172775
ID AAA17
XX AAA17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T7 promoter; ribosome binding site; RBS; prokaryotic; eukaryotic; ribosome; mRNA.circle-solid.polypeptide copolymer; mRcs.pC; SPERT Systematic Polypeptide Evolution by Reverse Translation; assay; diagnosis; cell sorting; inhibitor; probe; sequestering agent;
                                                                                                                                                                                                                                          Gold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligo #7 for cloning T7 promoter and RBS containing mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAI72775
                                                                                                                                                                                                                                                                                                                (GOLD/)
(TUER/)
(PRIB/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-NOV-1998;
02-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2002038000-A1
                                                                                Translation)) for specifically bind
                                                                                                         New methods (termed SPERT (Systematic Polypeptide Evolution by Translation)) for selecting high-affinity polypeptide ligands t
                                                                                                                                                                                       WPI; 2002-329128/36
                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-FEB-2001; 2001US-0790399.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAR-2002
                                                                                                                                                                                                                                                                                             (/TIMS
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                                                                                                                                                                                                                                                                                        GOLD L.
TUERK C.
PRIBNOW D.
SMITH J D.
                                                     drugs and receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTGCATGCAGAAGGACGGGWTGAAGGCGGACGGGATTGACGACGACGACGACATTGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               390 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACGACGACGACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACGAGGACGTCTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tuerk C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0197649.
90US-0561968.
91US-0739055.
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                                                                                selecting high-af target molecules,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA:
                                                                                                                                                                                                                                          Pribnow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45; DB
Pred. No. 0.02
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ۲,
                                                                                                                                                                                                                                          Smith JD
                                                                                   Ø
                                                                                g. proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22; Length 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56;
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                                                                                      carbohydrates,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                    Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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cc amplified to create candidate mixtures enriched in ribosome complexes. CC or mRcs.pCs with an affinity to the target, are new. The methods are cc termed SPERT (Systematic Polypeptide Evolution by Reverse Translation). CC The SPERT methods are useful for isolating polypeptide ligands for cd desired target molecules. The polypeptide products are useful for assay methods, diagnostic procedures, cell sorting, as inhibitors of cassay methods, diagnostic procedures, cell sorting, as inhibitors of target molecule function, as probes, as sequestering agents and the clike. In addition, polypeptide products of the invention can have catalytic activity. Target molecules include natural and synthetic cyplymers, including proteins, polysaccharides, glycoproteins, hormones, cc. receptors and cell surfaces, nucleic acids, and small molecules such as cdrugs, metabolites, cofactors, transition state analogues and toxins. CC receptors and cell surfaces, nucleic acids, and small molecules such as coldings, metabolites, cofactors, transition state analogues and toxins. CC polypeptides having a randomized amino acid sequence. Each member of ce mixture is linked to an individualized mRNA, which encodes the camino acid sequence of that polypeptides are portionally of binding to a given desired ce ach mRNA encoding to their property of binding to a given desired contantely, both the desired optimal polypeptide is partitioned together with the means for further amplifying it by an in vitro process. CC ultimately, both the desired optimal polypeptide is partitioned together with the means for further amplifying it by an in vitro process. CC desired, and further amplification of the coding sequence. It is cherefore not necessary to analyse the amino acid sequence of the indexired polypeptide (using protein chemistry) in order to produce it in desired polypeptide (using protein chemistry) in order to produce it is passived manner ties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a restriction endonuclease site. The resulting nucleic acid was used the method of the invention for preparing ligands of target molecules in which mixtures of ribosome complexes or mRNA.circle_solid.polypept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to make mRNA encoding a candidate polypeptide, a 5' fixed sequence composed of a T7 promoter sequence and a ribosome binding site which recognised by both prokaryotic and eukaryotic ribosomes, terminating
                                                   in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               copolymers (mRcs.pCs) are partitioned by affinity to the target and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequences given in AAI72769-81 are oligonucleotides which were
                                                             desired
                                                          quantities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ribosome complexes or mRNA.circle-solid.polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The resulting nucleic acid was used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used
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Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 other;

Score 45;

В 24;

Length

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                                                                              Matches
                                                                                   Query Match
Best Local
           141
121
                         61
                                      81
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                                                   μ.
                                                                              78;
                                                                                    Similarity
             ACGAGGACGTCTACG 155
                         GGTGCATGCAGAAGGACGGGWTGAAGGCGGACGGACGACGACGACGACGACGA
                                                                             Conservative
                                                                                  12.1%; 57.8%;
                                                                              <u>ب</u>
                                                                                    Pred.
                                                                              Mismatches
                                                                                    No. 0.021;
                                                                             56;
                                                                              Indels
                                                                              0
                                                                              Gaps
                                       140
                                                                  80
                          120
                                                    60
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## AAA30290 AAA30290 standard; DNA;

3489

ВP

11-SEP-2000 (first entry)

Kaposi's

RESULT 6
AAA3020
ID AAA33
XX
AC AAA3
XY
T11-S
XX
DT 11-S
XX
XX
DT 11-S
XX
Huma
KW Kapo
KW Huma
KW Kapo
KW Huma Kaposi's sarcoma-associated herpesvirus; KSHV; rhadino virus; latency-associated nuclear antigen; LANA; gamma-2 herpes virus; Human herpes virus 8; HHV8; rhadino virus cis-acting element; RVCAE;

sarcoma-associated herpesvirus LANA gene

Kaposi's primary effusion lymphoma; disease; ds

Example 1; Page 21; 38pp; English

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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rhadino virus infection is implicated in a variety of diseases e.g. Raposi's Sarcoma (KS), Primary Effusion Lymphoma (PEL) and multicentric Castleman's disease. In addition, KS is a common malignancy in HIV patients. KSHV persists in host cells in a latent form. One of the few genes expressed from the latent viral DNA is LANA, LANA associates with both human chromosomes and with the rhadino virus cis-acting element (RVCAE), thereby providing a tethering function: the KSHV DNA episome is "tied" to the host chromosomes. This allows the viral DNA to persist in the host cell. The present sequence may be used to screen and identify molecules that inhibit LANA interaction with RVCAE, thereby interfering with the latency cycle of this virus. Potential antiviral treatments for the both comparison of diseases may therefore he hadd on the first latency cycle of this virus. Potential antiviral treatments for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is the Kaposi's sarcoma-associated herpesvirus, (KSHV) latency-associated nuclear antigen (LANA) gene. KSHV is also as Human Herpes Virus 8 (HHV8) and belongs to the rhadino virus, or gamma-2 herpes virus class. The LANA protein is necessary for the efficient persistence of rhadino virus DNA in mammalian cells. Persi
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 6; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treating or preventing a disease associated with rhodino virus infection in a mammal which includes Kaposi's Sarcoma and Primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-387829/33.
P-PSDB; AAY96255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kieff ED,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KIEF/) KIEFF E D.
(BALL/) BALLESTAS M E.
(KAYE/) KAYE K M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200029626-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     above mentioned diseases may therefore be based on LANA deregulation
                                                                                                       1146
1206
                                                148
                                                                                                                                                       88
                                                                                                                                                                                                                                                            28
                                                                                                                                                                                                                                                                                                                                     Similarity
CG 1207
                                                :<u>ය</u>
                                                                                                       TGGGACCGCYGACGTCCTTGGCGGGGCGGAGCGCGAGAACCAAGACGACGAGGACGAGGA
                                                                                                                                                                                                        GGAGGATGACGAGGATGACGAGGATGACGAGGATGACGAGGAGGATGACGA
                                                                                                                                                                                                                                              GCAGAAGGACGGGWTGAAGGCGGACGGACGACGACGACGACATTGCGATGAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sarcoma-associated herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ballestas
                                                   149
                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0109422
99US-0298568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US27508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= b
/note= "nuclear localisation signal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product= "LANA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "nuclear localisation signal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190..210
                                                                                                                                                                                                                                                                                                                                                                                                                    1053 A; 862 C; 1137 G;
                                                                                                                                                                                                                                                                                                                                  11.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaye
                                                                                                                                                                                                                                                                                                                                     Score 43.2;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      爻
                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 437 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                              DB 21;
                                                                                                                                                                                                                                                                                                               49;
                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                              Length 3489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "SIN
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RESULT 7
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                                                                                                                                                                                                                               The invention provides a composition comprising nucleic acid, histone H1 protein and expression vector operationally encoding a protein suitable for tethering the nucleic acid to the histone H1 protein, where the ethering protein is LANA. The composition is useful in aiding the retention of the viral DNA in the host cell. The viral vector encodes a protein suitable for tethering DNA to Histone H1. Wethods for screening for compounds which are agonistic or antagonistic for the tethering of viral proteins to histone H1 and DNA binding sites are useful for developing the method of viral transfer. The composition has applications to gene therapy, including the treatment of multiple sclerosis, parkinson's disease, Huntington disease and diabetes. The present sequence represents the nucleotide sequence of the Kaposi's sarcoma associated herpesvirus (human herpesvirus 8) latency-associated nuclear antigen (LANA), which acts as a tethering protein.
                                                                                                                                                                                                          Sequence 3489 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 9A; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Histone H1; tethering protein; LANA; gene therapy; multiple sclerosis; Parkinson's disease; Huntington disease; diabetes; human herpesvirus 8 KSHV; latency-associated nuclear antigen; LANA; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF82901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF82901 standard; DNA; 3489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Robertson ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-SEP-2000; 2000WO-US26908.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200125484-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          composition for use in gene therapy comprises hat includes a nucleic acid sequence encoding
                                                                                                                                                               Local
                              1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-281736/29.
                                                          88
                                                                                                                                               72;
                                                                                                                                                               Similarity
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 CG 149
                              теерассесувансетссттеесеееееееееееееееееееееееее
                                                                                      GGAGGATGACGAGGATGACGAGGATGACGAGGATGACGAGGATGACGA
                                                                                                                   GCAGAAGGACGGGWTGAAGGCGGACGGACGACGACGACGACGACGATTGCGATGAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sarcoma associated herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence of KSHV tethering protein,
                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cotter MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0410399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..3489
                                                                                                                                                                                                        1053 A; 862 C; 1137 G; 437 T; 0 other;
                                                                                                                                                             11.6%;
59.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry.
                                                                                                                                              Score 43.2; Di
Pred. No. 0.11
1; Mismatches
                                                                                                                                               1;
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                                                                                                                                                               0.11;
                                                                                                                                                                            DB
                                                                                                                                                 49;
                                                                                                                                                                            22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          an expression vector a nucleic acid bindi
                                                                                                                                                  Indels
                                                                                                                                                                            Length 3489;
                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            binding
                                                                                                                                                 Gaps
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RESULT 8
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Matches 72
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                                                                                                                                                                         The present invention describes a system (A) for maintaining a plasmid as an episome in mammalian cells, comprising the rhadinoviral sequence LANA (latency-associated nuclear antigen) of 3489 base pairs (see ABA93487, S1) expressed in the cell, and the rhadinoviral sequence RVCAE (rhadinoviral cis-acting element) of 801 base pairs (see ABA93488, S2) present in the plasmid. Also describes is a method for maintaining a closed circular DNA in a cell by expressing (S1) in the cells and having (S2) as a cis-acting and maintenance sequence in the DNA. (A) is particularly used in gene therapy (or other gene transfer applications) that uses mammalian cells in which LANA is expressed. (A) improves persistence of gene therapy vectors in cells. The present sequence encodes Kaposi's sarcoma-associated herpesvirus (KSHV, also called human herpesvirus 8) LANA protein, which is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KSHV terminal repeat; rhadino virus cis acting element; episom primary effusion lymphoma; latency-associated nuclear antigen; gene therapy; gene transfer; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaposi's sarcoma-associated herpesvirus LANA protein encoding DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human herpesvirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kieff ED,
                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KIEF/)
                                                                                              Local Similarity
                              1086
                                                                                                                                                                                                                                                                                                                                                                                                  therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002-153769/20
                                                                                                                                                                                                                                                                                                                                                                       1.
                                                      28
  88
                                                                                   72;
                                                                                                                                                                                                                                                                                                                                                                                                 for episomal retention of plasmids in mammalian cells, herapy, comprises rhadinoviral LANA and RVCAE sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KIEFF
                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB05621
                                                                                                                                                                 invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sarcoma-associated herpesvirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                        3489
                                                                                                                                                                                                                                                                                                                                                                       Fig 6; 27pp; English
  TGGGACCGCYGACGTCCTTGGCGGGGCGGAGCGAGAACCAAGACGACGAGGACGAGGA
                            GGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGATGACGA
                                                      GCAGAAGGACGGGWTGAAGGCGGACGGGATTGACGACGACGACGACATTGCGATGAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ballestas
                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                        ₽P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "LANA protein"
/note= "latency-aggarian"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                      1053 A; 862 C; 1137 G; 437 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA;
                                                                                               11.6%;
59.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Œ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "latency-associated nuclear antigen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВР
                                                                                               Score 43.2; DB Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3
                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSHV;
                                                                                                              DB
                                                                                     49;
                                                                                                              24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LANA;
                                                                                                            Length 3489;
                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVCAE;
                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                 useful
                                                                                     Gaps
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88 TGGGACCGCYGACGTCCTTGGCGGGGGCGGAGCGAGGAACCAAGACGACGACGACGAGGACGA

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RESULT 9
AAV73805/c
ID AAV738
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                               Query Match
Best Local S
Matches 72
                                                                                                                                                                          This sequence is a fragment of the Kaposi's sarcoma-associated herpesvirus (KSHV) LUR (long unique region). This fragment contains coding regions for ORF65 which encodes capsid protein IV, ORF66, ORF67 which encodes tegument protein IV, ORF68 which encodes a glycoprotein, ORF69, K12 which encodes kaposin, K13, ORF72 which encodes cyclin D, ORF73 which encodes kaposin, K13, ORF72 which encodes ox-2 (v-adh), ORF74 which encodes G-protein coupled receptor, ORF75 which encodes tegument protein/FGARAT, K15. KSHV is a new human herpesvirus (HHV8) believed to cause Kaposi's sarcoma (KS) which is the
                                                                                                                                                                                                                                                                                                                                          Kaposi's sarcoma-associated herpes virus nucleic acid - di:hydro:folate reductase and is useful for treatment, I or diagnosis of Kaposi's sarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dihydrofolate reductase; LUR; long unique region; vaccine; diagnosis; treatment; HHV8; capsid protein IV; tegument proglycoprotein; kaposin; cyclin D; immediate early protein; v-adh; G-protein coupled receptor; FGARAT; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV73805 standard;
                                                                                                        most common form of neoplasm occurring in persons with deficiency syndrome (AIDS). The DHFR protein is useful prophylaxis, diagnosis and treatment of a subject with and for detecting expression of a DNA virus associated sarcoma in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KSHV LUR
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-069741/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5849564-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kaposi's sarcoma-associated herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaposi's sarcoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV73805;
                                                                                                                                                                                                                                                                                                                                                                                                                          Bohenzky RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998
                                                                                   Sequence 32207
                                                                                                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYCO ) UNIV
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       28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ရှ:
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ය
GCAGAAGGACGGGWTGAAGGCGGACGGACGACGACGACGACGATGGCGATGAAAGA
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                                                                                                                                                                                                                                                                                                                   Column 155-182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (nucleotides 105,301-137,507).
                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                         Chang Y,
                                                                                      BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acquired immune deficiency syndrome; AIDS; DHFR; Bcl-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA; 32207
                                                                                      7229
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                                              11.6%;
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                                                                                      9156 C;
                                                                                                                                                                                                                                                                                                                   109pp;
                                 Score 43.2; D
Pred. No. 0.18
1; Mismatches
                                                                                                                               occurring in persons with acquired immune of the DHFR protein is useful for vaccination, reatment of a subject with Kaposi's sarcoma of a DNA virus associated with Kaposi's
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                                                                                       8713 G;
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                                              .18;
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                                                                                                                                                                                                                                                                                                                                                              treatment, prophylaxis
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                                                           Length 32207;
                                      Indels
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RESULT 10
AAV19941/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaposi's sarcoma-associated herpes virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interleukin-6; IL-6; interferon regulatory factor; rheumatoid arthritis; complement-binding protein; glycoprotein; capsid protein IV; infection; immediate early protein; Kaposi's sarcoma; protective vaccine; lymphoma; lymphoproliferative disease; leukaemia; splenomegaly; mycosis fungoides;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KSHV; HHV8; human herpes virus 8; macrophage inflammatory protein II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSHV long unique coding region and terminal repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immune status; anti-inflammatory agent; therapy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                /product= interleukin 6
complement (21548..21832)
                                                                                                                                                                                                                                                                                                                                                                                                               /product= glycoprotein B
complement (17261..17875)
                                                                                                                                                                                                                      complement
                                                           product= capsid protein IV (23808..127296)
                                                                                        product= interferon regulatory factor complement (111931...112443)
                                                                                          complement
                                                                                                                         complement
                                                                                                                                                                                                                                                     /product= glycoprotein M
complement (69412..69915)
                                                                                                                                                                                                                                                                                    product= protein T1.1 (58976..60175)
                                                                                                                                                                                                                                                                                     complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        location/Qualifiers
                                     product= immediate early protein
                                                                                                                        product= glycoprotein X complement (93636..94127)
                                                                                                                                                                                                                     product= glycoprotein L
complement (88410..88910)
                                                                                                                                                                                                                                                                                                                          roduct= interferon regulatory factor
                                                                                                                                                                                                                                                                                                                                                   product= macrophage inflammatory protein II
complement (27137...27424)
                                                                                                                                                                 product= interferon
                                                                                                                                                                                                product= interferon regulatory factor
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RESULT 11 AAV64956 ID AAV64

AAV64956 standard; DNA; 150 BP.

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                                                                                                                                                                                                                                                                              encoded by ORF73. Labelled probes for the nucleic acid, proteins encoded by it, and antibodies (Ab) specific for the proteins are useful for detecting HHV8, specifically for diagnosis of Kaposi's sarcoma, in body fluids or tissue samples. HHV8 infections can be treated with antisense or triplex forming molecules or agents that bind specifically to the protein. Ab may be used for prophylaxis or treatment of HHV8 infection, while the protein can be used in protective vaccines. Ab may also be used to differentiate between lymphomas, and HHV8 may be implicated in many cother lymphoproliferative diseases such as lymphomas, leukaemia, containing and mycosis fungoides. Cells and animals containing the nucleic acid are useful for drug screening. HHV8-derived peptides can be used as targets for antiviral drugs, e.g. dihydrofolate reductase gene can be inhibited with methorreate. These can also be used to determine the inmune status of a patient infected with HV. HHV8 derived protein coviral MIP III may be used as an anti-inflammatory agent for, e.g. treating rhemmatoid arthritis. This sequence is stated as containing
                                                                                                                                                                                                           Matches
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25-JUL-1996;
25-JUL-1996;
25-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the long unique region and terminal repeat of the Kaposi's sarcoma-associated herpes virus (KSHV). KSHV is also known as human herpes virus 8 (HHV8). This sequence contains the DNAs of the invention which encode KSHV polypeptides selected from: (a) viral macrophage inflammatory protein (MID II; (b) viral interleukin-6 (IL-6); (c) viral IRF 1; (d) complement-binding protein; glycoproteins B, M or L; (d) capsid protein IV encoded by ORF65; and (e) immediate early protein encoded by ORF73. Labelled probes for the nucleic acid, proteins encoded
                                                                                                                                                                                                                                                                            Sequence 137507 BP; 32579 A; 37795 C; 35758 G; 31375 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding Kaposi's sarcoma associated he proteins - useful for, e.g. detecting levels of HHV8 in, preparation of vaccines for treatment of, HIV patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-130615/12
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25-JUL-1996;
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13-NOV-1996;
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                                                                                                                                                                                                         72;
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                                                                                                                                                                 GCAGAAGGACGGGWTGAAGGCGGACGGACGACGACGACGACGACATTGCGATGAAAGA
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                                                                                                                                    GGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGATGACGAGGAGGATGACGA
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ရှ
                                                                   TGGGACCGCYGACGTCCTTGGCGGGGCGGAGGGGCGAGGAGCGAGGACGAGGA
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                                149
126090
                                                                                                                                                                                                           Conservative
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96US-0686350
96US-0687253
96US-0688114
96US-0708678
96US-0728323
96US-0747887
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96US-0686243
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                                                                                                                                                                                                                        11.6%;
59.0%;
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                                                                                                                                                                                                                         Score 43.2;
Pred. No. 0
                                                                                                                                                                                                         Mismatches
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in, and
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RESULT 12
AAH74202
ID AAH74
XX AAH74
XX AAH74
XX IS-OC
DT 15-OC
DX Nucle
XX Nucle
XX OS Vario
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Best Local S
Matches 73
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02-AUG-1990;
01-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ligand; assay; diagnostic; inhibitor; probe; cell sorting; catalysis;
                                                                                                                                                                                                                                                                                                           AAV64950-V64972 are sequences used in a method for the production of a polypeptide ligand of a target molecule. The polypeptide products can be used in assays, in diagnostic procedures, in cell sorting, as inhibitors of target molecule function, as probes, as sequestering agents, or may have catalytic activity.
                                                                                                                                                                                                                                                                                                                                                                                  Production of polypeptide ligands using mRNA-polypeptide conjugates - by affinity selection, RNA amplification and polypeptide synthesi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JAN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequestering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse histone
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                                                                                                                                                                                                                                                                                                                                                                   Example 10;
         Varicella virus
                         Oka strain; pox vaccine; vaccine; poxvirus disease; chickenpox;
                                            Nucleotide
                                                               15-OCT-2001
                                                                                                 AAH74202 standard;
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                                                                                                                                                               TACGC 156
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                                                                                                                                                                                                                                                                                                                                                                   Column 45-46;
                                           sequence
                                                                                                                                                                                                                                                         Conservative
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                                                               (first
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90US-0561968.
91US-0739055.
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                                                                                                                                                                                                                                                                                           44 A; 46 C;
                                                                                                 DNA; 125157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epitope; ss.
                                            of.
                                                               entry)
                                                                                                                                                                                                                                                                 11.6%;
58.4%;
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                                             the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epitope
                                                                                                                                                                                                                                                                                                                                                                   35pp; English.
                                            Varicella virus Oka strain
                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                        Score 43; DB:
Pred. No. 0.05
1; Mismatches
                                                                                                                                                                                                                                                                                            53 G; 6 T;
                                                                                                  ВP
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م.057;
                                                                                                                                                                                                                                                                                             1 other;
                                                                                                                                                                                                                                                          51;
                                                                                                                                                                                                                                                                         Length 150
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RESULT 1:
AAC78059
ID AAC78059
AC AACY
XX AACY
AC AACY
XX Hum
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KW dia.
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the DNA sequence of specific parts of the viral genome in a sample is determined and proved to be conserved rather than mutated in comparison with the same parts of a reference viral genome. The method is useful for quality control of vaccines for use in the prevention of poxvirus
                                                                                                                                                         diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antiinflammatory; antithyroid; antialtergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents the nucleotide sequence of Varicella virus, Oka strain. The specification describes a method for the quality control of an attenuated pox vaccine, characterised in that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Method for checking absence of mutation at varicella virus genome for quality control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JAN-2001; 2001WO-JP00678
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                                                                                                                                                                                                                                                                                                                                                                                 Human; cancer associated gene; cancer antigen; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cancer associated gene sequence SEQ ID NO:453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC78059;
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                                                                               Homo sapiens.
                                                                                                                                  neurological
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                                                                                                                                        disease;
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58.4%;
                                                                                                                                        drug
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                                                                                                                                        screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or inhibiting the prolliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. ARC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antinflammatory; antithyroid; antiallergic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosting pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating
                                Drosophila; development pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in AAB43398 to AAB44239. The proteins can have activities based on tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acids comprising sequences encoding useful for treating or diagnosing e.g. cancer - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-587533/55.
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   Drosophila melanogaster
                                                                                       Drosophila
                                                                                                                         26-MAR-2002
                                                                                                                                                            ABL13753
                                                                                                                                                                                            ABL13753 standard; cDNA; 3111 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC77607
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                                                                                                                                                                                                                                                                                 1208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to AAC78448 encode the human cancer associated proteins given 398 to AAB44239. The proteins can have activities based on the
                                                                                                                                                                                                                                                                                                                    AC
                                                                                                                                                                                                                                                                                                                                                                                     CCGCYGACGTCCTTGGCGGGGGGGGAGCGAGGAAACCAAGACGACGAGGACGAGGACGTCT
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                                                                                                                                                                                                                                                                                                                                                      CAGCAGCAGTGGTGGATGTGGCGGAGGGAGGAGGAGAGAGGAGAATGAGGACCTCT
                                                                                     melanogaster expressed polynucleotide SEQ ID NO 35741
                                                                                                                                                                                                                                                                                                                    154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention.
                                                  developmental biology; cell signalling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP; 491 A; 657 C; 654 G;
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Pred. No.
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                                                    insecticide;
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RESULT 15
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           capable of detecting 1000 or more genes from Drosophila. The invuseful in developmental biology and in elucidating cell signallicell-cell interactions in higher eukaryottes for the development insecticides, therapeutics and pharmaceutical drugs. The inventi discloses genomic DNA sequences (ABL16176-ABL30511), expressed Discussions (ABL01840-ABL16175) and the encoded proteins
CDS
                                                            Human; cell regulatory protein; p193; apoptosis associated BH3 domain; cell cycle; cardiomyocyte; tumourogenic cell; apoptotic activity; cell proliferation; anti-apoptotic; myocardial infarct; cardiomyopathy; cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ABB57737-ABB72072).
The sequence data for this patent did not form specification, but was obtained in electronic f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 35741; 21pp + Sequence Listing; English.
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11-JUL-2000; 2000US-0614150
                                     ното
                                                                                                                             Human cell regulatory protein p193 cDNA.
                                                                                                                                                       09-MAY-2001
                                                                                                                                                                                                          AAS00419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent
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                                                                                                                                                                                                        standard;
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                                                                                                                                                     (first
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Location/Qualifiers 87..5183
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                                                                                                                                                                                                        cDNA; 5253
                                                                                                                                                       entry)
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57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                               2;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42;
Pred. No.
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format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3111;
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                                                                                                   protein;
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Search completed: September 14, 2003, 23:24:02 Job time : 224 secs
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                                                                                                                                                                                                                                                                                                                                                                          The present sequence encoding for novel human cell regulatory protein CC is an apoptosis-associated protein comprising a BH3 domain (AAU00417). CC A homologous mouse p193 protein (AAU00415) is also described. The p193 protein is useful as a target for modifying the G1 phase of the cell cycle of a mammalian cell, preferably human and for inducing apoptosis CC in an inappropriately proliferative cell. A nucleic acid encoding p193 is CC polynucleotide sequence into mammalian or other eukaryotic cells such as CC cardiomycoytes, hepatocytes, smooth muscle cells, haematopoietic stem CC cardiomycoytes, hepatocytes, smooth muscle cells, haematopoietic stem CC is useful in the study and understanding of the cell cycle, in screening CC aspects of the cell cycle, or in the culture of cells naving suppressed apoptotic activity and/or increased proliferative potential for cardiomycoytes or a mixture of all these cells are genetically modified CC acids which are delivered to the subjects in a damaged or diseased area of the heart in cases of myocardial infarcts and cardiomyopathies.
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Best Local S
Matches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New apoptosis-associated p193 protein, used as a target for modifying the cell cycle involving modifying the p193 protein level and/or interfering with the p193 signal transduction pathway to induce or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-218429/22.
P-PSDB; AAU00416.
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                                                                                                                                                                                                                                                                                                                                                 Sequence 5253 BP; 1109 A; 1531 C; 1564 G; 1049 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    suppress apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ADRE-) ADVANCED RES & TECHNOLOGY INST.
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                                                                      4228 AC 4229
                                                                                                                                                                                                            4168 CAGCAGCAGTGGTGGATGTGGCGGAGGGAGAGGAGGAGGAGGAGGAGGACCTCT
                                                                                                        153
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-09-288-568-1
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9465, Ap
9317, Ap
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APPLICANT: Gold, Larry
APPLICANT: Tuerk, Craig
APPLICANT: Tuerk, Craig
APPLICANT: Smith, Jonathan D.
TITLE OF INVENTION: Systematic Polypeptide Evolution by
FILE REFERENCE: NEXO2/C1-CON
CURRENT APPLICATION NUMBER: US/09/197,649
CURRENT FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: 07/829,461
EARLIER FILING DATE: 1992-01-31
EARLIER FILING DATE: 1992-08-03
EARLIER APPLICATION NUMBER: 07/739,055
EARLIER APPLICATION NUMBER: 07/561,968
EARLIER APPLICATION NUMBER: 07/561,968
EARLIER FILING DATE: 1990-08-02
NUMBER OF SEQ ID NOS: 26
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Best Local Similarity
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CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1931
TYPE: DNA
ORGANISM: EBNA
                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 7
LENGTH: 390
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Patent No. 6194550
                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: Sequence OTHER INFORMATION: having a 120 repeat of ACG flanked by fixed OTHER INFORMATION: fragments having NCOI restriction sites.
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PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 9337
LENGTH: 918
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: MAYC J. Rubenfield et al.
APPLICANT: MAYC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO A.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTI
FILE REFERENCE: 107106.136
CURRENT FILING DATE: 1999-02-18
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 9465
LENGTH: 789
TYPE: DNA
DRGANISM: Besudomonas aeruginosa
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                                                                                                                 Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9337, Application US/09252991A Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MATC J. RUBERFIELD et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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Similarity 53.5%;
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                 11.7%;
53.5%;
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                                                                                                                 Score 43.4; DB 4; Pred. No. 0.0072; 3; Mismatches 69;
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Pred. No. 0.0069)
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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 9411
LENGTH: 1440
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US-08-728-323A-1
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Best Local Similarity
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Patent No. 6551795
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                               APPLICANT: Edelman, Isidore APPLICANT: Moore, Patrick S. TITLE OF INVENTION: Immediat TITLE OF INVENTION: Sarcoma-TITLE OF INVENTION: Encoding
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                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                      ADDRESSEE: Cooper & Dunham LLP STREET: 1185 Avenue of the Americas CITY: New York
                                                                                                                                 COUNTRY: U.S.A.
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Russo, James J.
Edelman, Isidore S.
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                                                                                                                                                                                                                                                                                          Sarcoma-Associated Herpesvirus
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Pred. No. 0.0083;
3; Mismatches 6
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                                                                                                                                                                                                      ; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-298-568-1
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                                                                                                                                                                                                                                                      SEQ ID NO 1
LENGTH: 3
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Best Local
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APPLICANT: Ballestas, Mary E.
APPLICANT: Ballestas, Mary E.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 632279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09298568
                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US/09/298,568
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                      TYPE: DNA
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 05
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mes 72; Conserv
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 3489 base pairs
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1086 GGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGATGACGAGGAGGATGACGA 1145
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                                                                                                                                                                                                                                                        3489
                                                                                                                                h 11.6%;
Similarity 59.0%;
72; Conservative
                     GCAGAAGGACGGGWTGAAGGCGGACGGACGACGACGACGACATTGCGATGAAAGA 87
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                                                                                                                              Score 43.2; DB Pred. No. 0.012; Mismatches
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Pred. No. 0.012;
1; Mismatches 49;
                                                                                                                                                                DB 4;
                                                                                                                                    49;
                                                                                                                                                                Length 3489;
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US-08-770-379-20/c
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Patent No. 6482587
GENERAL INFORMATION:
APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence 20, Application US/08770379
Patent No. 5849564
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TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
TITLE OF INVENTION: to Genomic Host DNA
FILE REFERENCE: UM-03778
CURRENT APPLICATION NUMBER: US/09/410,399
CURRENT FILING DATE: 1999-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: Chang, Yuan

APPLICANT: Bohenzky, Roy A.

APPLICANT: Russo, James J.

APPLICANT: Beelman, Isidore S.

APPLICANT: MOOTE, PATTICK S.

APPLICANT: MOOTE, PAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 3489
                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                  FILING DATE:
CLASSIFICATION:
                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1206
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                                                                                                        US/08/770,379

    Mismatches

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GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212) 278-04(
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                         TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4518
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: White, John P.
REGISTON NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,669
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
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                                                                 TELEPHONE: (212) 7
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TYPE: nucleic acid
                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
ZIP: 10036
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 LENGTH: 3220 acid
STRANDEDNESS:
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Y: U.S.A.
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                            32207 base pairs
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Russo, James J.
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Pred. No. 0.024;
1; Mismatches
                                                                                                                             45185-F
                                                                                                                                                                                                                                                           Version #1.30
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; LENGTH: 32207
; TYPE: DNA
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-230-371A-20
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APPLICANT: Bohenzky, Roy A
APPLICANT: Bohenzky, Roy A
APPLICANT: Bdelman, Isidore S
APPLICANT: Bdelman, Isidore S
APPLICANT: Moore, Patrick S
TITLE OF INVENTION: UNIQUE ASSOCIA-
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 45185-G-PCT-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-230-371A-20/c
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Best Local Similarity 59.0
                                                                                        Sequence 8, Application US/07829461A Patent No. 5843701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20, Application US/09230371A Patent No. 6348586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 45185-G-PCT-US
CURRENT APPLICATION NUMBER: US/09/230,371A
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: PCT/US97/13346
PRIOR FILING DATE: 1997-07-22
NUMBER OF SEQ ID NOS: 30
                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
            APPLICANT: Gold, Larry
TITLE OF INVENTION: Sy:
TITLE OF INVENTION: Eve
TITLE OF INVENTION: Tri
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                 CG 149
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                                                                                                                                                                                                                                                                                                                                                                                     11.6%;
59.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES
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59.0%;
                Trnslation
                           Systematic Polypeptide
Evolution by Reverse
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                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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GENERAL INFORMATION:

APPLICANT: MARC J. Rubenfield et al.

APPLICANT: MARC J. RUBENFIELD AND AMINO ACID SEQUENCES RELATING TO I

TITLE OF INVENTION: ACCUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION UNMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 1663

LENGTH: 1146
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TOPOLOGY:
US-07-829-461A-8
                                                                                                                                                                                                                                                                                      Sequence 10603, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/739,055
FILING DATE: 01-AUGUST-1991
PRIOR APPLICATION DATA: 7968
APPLICATION NUMBER: 07/561,968
FILING DATE: 02-AUGUST-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (303) 850-941 INFORMATION FOR SEQ ID NO:
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 150 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: (303) 850-9900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/829,461A
FILING DATE: January 31, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADUNESSEE: Beaton & Swanson, P.C.
STREET: 4582 South Ulster Street Parkway, #403
CITY: Denver
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Barry J. Swanson REGISTRATION NUMBER: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM CON
OPERATING SYSTEM:
SOFTWARE: WORDPOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                            126 · GACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 TACGC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 AAGGACGGGWTGAAGGCGGACGGGATTGACGACGACGACGACATTGCGATGAAAGATGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Pred. No. 0.0053;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51;
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**PSEUDOMONAS** 

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APPLICANT: MAIC J. Rubenfield et al.

APPLICANT: MAIC J. Rubenfield acid sequences relating to pseudomonas;

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS;

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 10250

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-10250
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Sequence 10250, Application US/09252991A

Patent NO. 6551795

GENERAL INFORMATION:
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US-09-252-991A-10603
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Search completed: September 15, 2003, 00:34:50 Job time : 56 secs
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Best Local Similarity 53.4%;
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                   y Match 11.1%; Score 41.2; DB 4; Length 1260;
Local Similarity 53.4%; Pred. No. 0.032;
hes 79; Conservative 3; Mismatches 66; Indels 0
                                                                                                                                                                                                                                        1105 GGTTCTGGGGGTTGAGCGTGGCGCCAGCGAGGCGGACCTGAAGAAGGCCCTACCGCCGCCT 1046
                                                                                                                                                            1045 GGCGATGAAATATCACCCGGACCGCAATCCTGGCGACAAGGAAGCCGAGGACAAGTTCAA 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 CGAGGACGAGGACGTCTACGCGCGCATC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 GGÁGGCCAÁCGÁGGCCTÁCGAGGTCCTC 183
                                                                                                                       136
                                                                               985 GGAGGCCAACGAGGCCTACGAGGTCCTC 958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 GGCGATGAAATATCACCCGGACCGCAATCCTGGCGACAAGGAAGCCGAGGACAAGTTCAA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 GETTETGGGGGTTGAGCGTGGCGCCAGCGAGGCGGACCTGAAGAAGGCCTACCGCCGCCT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 SGCTCGGTGCATGCAGAAGGACGGGWTGAAGGCGGACGGACGACGACGACGACGACAT 75
                                                                                                                                                                                                                                                                   CGAGGACGACGTCTACGCGCGCATC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41.2; DB 4; Length 1146; Pred. No. 0.031; 3; Mismatches 66; Indels 0
                                                                                                                                                                                                                                                                                                                         0;
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Run
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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43.2
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                                                                                                                                                                                                                                                                                                                                           369
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                              Query
Match Length
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Gapop 10.0 , Gapext 1.0
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                                                                                      99.5 371
98.8 390
11.6 3489
11.6 125157
11.3 470
11.3 2254
11.3 5253
11.3 5253
11.3 1437
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1 12 US-09-849-729-1

12 US-09-849-729-2

12 US-09-790-399-7

12 US-11-294-804-1

11 US-09-913-514-23

11 US-09-913-514-23

11 US-09-913-914-853

10 US-09-925-301-453

10 US-09-980-107-1655

11 US-09-880-107-1655

14 US-10-080-944-3

19 US-09-815-242-7738

10 US-09-815-242-7738

11 US-10-156-761-2598

12 US-09-913-514-31

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Sequence 1, Appli
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Sequence 23, Appli
Sequence 2891, A
Sequence 453, Appli
Sequence 453, App
Sequence 1655, Ap
Sequence 7738, Ap
Sequence 7738, Ap
Sequence 2598, Ap
Sequence 20, Appli
Sequence 31, Appli
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	9.9	9.9	10.0	10.0	10.1	10.1	10.1	0	0	0	10.2	10.2	0	10.2	10.4	10.4	0	10.4	10.4	10.4	10.5	10.5	10.5	0	10.5	0.6	10.6	10.7
1886	1560	575	2817	477	1294	1869	1235	4548	9025608	1223197	1885	1429	861	573	5169	5168	3169	3169	3000	2946	124884	124884	434	306	1341	9	1389	5387
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US-09-373-658-36	US-10-156-761-5073	US-09-864-761-20733	US-10-037-270-1085	US-10-156-761-5780	US-10-151-832-4	US-10-156-761-3570	US-09-925-301-143	US-10-156-761-6166	US-10-156-761-1	US-10-027-632-179264	US-10-106-698-420	US-10-198-846-13550	US-10-156-761-3690	US-10-156-761-5782	US-10-128-714-5364	US-10-128-714-364	US-10-128-714-6364	US-10-128-714-1364	US-10-128-714-2364	US-10-128-714-7364	US-10-288-823-76	US-09-913-514-1	US-09-960-352-2292	US-09-913-514-32	US-10-156-761-4629	US-10-175-523-97	US-10-156-761-5431	US-10-001-873-22
36, ĀĮ	e 5073,	N	1085,	Sequence 5780, Ap	Sequence 4, Appli	Sequence 3570, Ap	Sequence 143, App	Sequence 6166, Ap	Sequence 1, Appli	e 17	Sequence 420, App	13550,	3690,	5782,	5364,	~	6364,	1364,		73	76	e 1, 7	22	32,	Sequence 4629, Ap	97,	Sequence 5431, Ap	Sequence 22, Appl

## ALIGNMENTS

```
APPLICANT: Lewis Samantha
APPLICANT: Batz, Hans-Georg
APPLICANT: Ramaswamy, Latha
APPLICANT: Bohenzky, Roy
APPLICANT: Lin, Yu-Huei
APPLICANT: Montiel, Janine
APPLICANT: Chen, Beniamin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/0984;
Publication No. US20030165540A1
GENERAL INFORMATION:
APPLICANT: Liu, Jen-Kuei
APPLICANT: Lewis, Samantha
APPLICANT: Lewis, Samantha
                                                                                                                                                                           Query Match 99.5%; Score 369; DB 12; Length 37 Best Local Similarity 100.0%; Pred. No. 2.5e-105; Matches 371; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                       SEQ ID NO 1
LENGTH: 371
TYPE: DNA
ORGANISM: Sentinel Virus II
                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Sentinel Virus II
FILE REFERENCE: RDID 0070
CURRENT APPLICATION NUMBER: US/09/849,729
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/202271
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.0
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                                                                                                            1 GATCMGGAAACGYTTSGCTCGGTGCATGCAGAAGGACGGGWTGAAGGCGGACGGGATTGA 60
                     GATCMGGAAACGYTTSGCTCGGTGCATGCAGAAGGACGGGWTGAAGGCGGACGGGATTGA
CGACGACGACATTGCGATGAAAGATGGGACCGCYGACGTCCTTGGCGGGGGGGGAGCG
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Gaps

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41.8 41.6 41.6 40.4 40.4 39.8

11.2 9025608 10.9 228 : 10.9 659158 : 10.7 494 :

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NAME/KEY: misc_feature
LOCATION: (372)...(372)
OTHER INFORMATION: unknown: can be a, t, g, c
OTHER INFORMATION: in this position.
US-09-849-729-2
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CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/202271
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09849729
Publication No. US20030165540A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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APPLICANT:
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                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Montiel, Janine
APPLICANT: Chen, Benjamin
TITLE OF INVENTION: Sentinel Virus II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Liu, Jen-Kuei
APPLICANT: Lewis, Samant
APPLICANT: Batz, Hans-G
APPLICANT: Ramaswamy, La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: RDID 0070
                                                                                                                                                                                                                                                                                                                                         LENGTH: 372
TYPE: DNA
ORGANISM: Sentinel Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241
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                                                                                                                                     GATCMGGAAACGYTTSGCTCGGTGCATGCAGAAGGACGGGWTGAAGGCCGGACGGGATTGA
                            GGTATTTGACACCTCCGCATTGCTGATCCTGAAGTTCTCGCTTGCAGACGCCTGATTCAGC
                                                                                                                CGACGACGACATTGCGATGAAAGATGGGACCGCYGACGTCCTTGGCGGGGGGGGGAGCG
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Batz, Hans-Georg
             GGTATTTGACACCTCCGCATTGCTGATCCTGAAGTTCTCGCTTGCAGACGCTGATTCAGC
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Bohenzky, Roy
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Pred. No. 1.4e-104;
0; Mismatches 2;
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US-09-790-399-7
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                                                                 Sequence 1, Application US/10294804; Publication No. US20030133948A1; GENERAL INFORMATION:
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US-10-294-804-1
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                                                                                                                                                                                                                                                                                                                         Query Match
Best Local 9
  APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or Enhance
TITLE OF INVENTION: to Genomic Host DNA
FILE REFERENCE: UM-03778
                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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GENERAL INFORMATION:

APPLICANT: Gold, Larry
APPLICANT: Gold, Craig
APPLICANT: Tuerk, Craig
APPLICANT: Pribnow, David
APPLICANT: Pribnow, David
APPLICANT: Smith, Jonathan D.
FILE REFERENCE: NEXO2/C1-CON2
CURRENT APPLICATION NUMBER: US/09/790,399
CURRENT APPLICATION NUMBER: 09/197,649
PRIOR APPLICATION NUMBER: 07/87,649
PRIOR APPLICATION NUMBER: 07/829,461
PRIOR APPLICATION NUMBER: 07/829,461
PRIOR APPLICATION NUMBER: 07/829,461
PRIOR APPLICATION NUMBER: 07/829,461
PRIOR APPLICATION NUMBER: 07/739,055
PRIOR APPLICATION NUMBER: 07/739,055
PRIOR APPLICATION NUMBER: 07/561,968
PRIOR FILING DATE: 1991-08-01
PRIOR APPLICATION NUMBER: 07/561,968
PRIOR FILING DATE: 1990-08-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: Sequence; OTHER INFORMATION: having a 120 repeat of ACG flanked by fixed; OTHER INFORMATION: fragments having NcoI restriction sites. US-09-790-399-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09790399 Patent No. US20020038000A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 390
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                         Similarity 57.
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ACGACGACGACGACG
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                                                                                                                                                                                          12.1%; 57.8%;
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Pred. No. 0.0003;
1; Mismatches 56;
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; Sequence 23, Application US/09913514
; Publication No. US20030082210A1
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SQQ ID NO 23
LENGTH: 261
TYPE: DNA
ORGANISM: Varicella virus
                                                                                                                                                                                                          Query Match
Best Local
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APPLICANT: SUNAV
APPLICANT: TAKAH
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LENGTH: 3489
                                                                                                                                                                                              Matches
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NAME/KEY: misc feature
LOCATION: (1). [261)
OTHER INFORMATION: Attenuated Oka strain
-09-913-514-23
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APPLICANT: TAKAHASHI, Michiaki
APPLICANT: TAKAHASHI, Michiaki
APPLICANT: YAMANISHI, Koichi
TITLE OF INVENTION: Method for Quality Control of an Attenuated Varicella Live Vaccir
FILE REFERENCE: 0216-0454P
CUURENT APPLICATION NUMBER: US/09/913,514
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: PCT/JP01/00678
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: JP 2000-62734
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR SEQ. ID NOS: 42
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PRIOR FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
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CURRENT FILING DATE: 2002-11-14
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ORGANISM: Kaposi's sarcoma-associated herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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ACGCG
                                ACGCG
                                                              CCGCYGACGTCCTTGGCGGGGCGGAGCGAGGAACCAAGACGACGAGGACGAGGACGTCT 152
                                                                                                                             AGGACGGGWTGAAGGCGGACGGGATTGACGACGACGACGACGACATTGCGATGAAAGATGGGA 92
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                                                                                                                                                                                           11.6%; ilarity 58.4%; Conservative
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232
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Pred. No. 0.00:
1; Mismatches
                                                                                                                                                                                                         Score 43;
Pred. No.
                                                                                                                                                                                        ed. No. 0.0012;
Mismatches 5
                                                                                                                                                                                                                         DB 11; Length 261;
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; Sequence 2, Application US/09913514
; Publication No. US20030082210A1
; GENERAL INFORMATION:
; APPLICANT: GOMI, Yasuyuki
; APPLICANT: SUNAMACHI, Hiroki'
; APPLICANT: TAKAHASHI, Michiaki
; APPLICANT: YAMANISHI, Koichi
; APPLICANT: YAMANISHI, Koichi
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US-09-918-995-28591
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                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: HYSEQ, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
                                                                                                                             NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 28591
LENGTH: 470
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 28591, Application US/09918995 Publication No. US20030073623A1
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CURRENT APPLICATION NUMBER: US/09/913,514
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: PCT/JP01/00678
PRIOR PILING DATE: 2001-01-31
PRIOR PILING DATE: 2001-01-31
PRIOR FILING DATE: 2000-01-31
                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US/09/235,076 PRIOR FILING DATE: 1999-01-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (1)...(125157)
OTHER INFORMATION: Attenuated Oka strain
            NAME/KEY: misc_feature
LOCATION: (1)...(470)
OTHER INFORMATION: n =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Varicella
                                                                                       ORGANISM: Homo sapiens
                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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58.4%;
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Pred. No. 0.0043;
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PRIOR APPLICATION NUMBER: PCT/US00/05882

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 453

LENGTH: 2254
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; ORGANISM: Homo sapiens
US-09-925-301-453
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US-09-925-301-453
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Best Local S
Matches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
                                                                                                                                                                                  Sequence 1655, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 453, Application US/09925301 Patent No. US20020052308A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                        APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expession Profiles
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
CURRENT FILING DATE: 2001-06-14
                                                                                                                                     APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Josep
APPLICANT: Scherf, Uwe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR PRIOR
                             PRIOR APPLICATION NUMBER: US 60/211,379 PRIOR FILING DATE: 2000-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity nes 72; Conserv
                APPLICATION NUMBER: US 60/237,054
 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                             1148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72;
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                                                                                                                                                                                                                                                                                                                                                                                          CCGCYGACGTCCTTGGCGGGGGGGAGCGCGAGAACCAAGACGACGAGGACGAGGACGTCT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGCAGCAGTGGTGGATGTGGCGGAGGGAGGAGGAGGAGGAGGAGGAGGAGGACCTCT
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                                                                                                                                                                                                                                                                                                 AC 1209
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Scherf, Uwe
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 2000-10-02
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Pred. No. 0.0027;
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                                                                                                            in Liver Cancer
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RESULT 10
US-10-080-943-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/10080943
Publication No. US20030073236A1
GENERAL INFORMATION:
APPLICANT: Field, Loren J.
APPLICANT: Tsai, Shib-Chong
TITLE OF INVENTION: p193 PROTEINS AND NUCLEIC ACIDS, AND USES THEREOF
FILE REFERENCE: IU99-PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 1655
LENGTH: 5253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity Matches 72; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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SOFTWARE: PatentIn Ver. 2.1
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CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 60/150,266
PRIOR FILING DATE: 1999-08-23
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: (87)..(5183)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens FEATURE:
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Similarity 59.0%;
                                                            AC 154
                                                                                                                           CAGCAGCAGTGGTGGATGTGGCGGAGGGAGGAGGAGGAGGAGGAGGAGGACCTCT
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   4229
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Pred. No.
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RESULT 11 US-09-815-242-7738/c

Sequence 7738, Application US/09815242 Patent No. US20020061569A1

GENERAL

INFORMATION

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RESULT 12
US-10-156-761-2598
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; NAME/KEY: CDS
; LOCATION: (1)...(1437)
US-09-815-242-7738
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SKIBA, TADAYOSHI
APPLICANT: HATTORI, WASAHIRA
TITLE OF INVENTION: WOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION UNMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
                                                                                                                                                                                                                                        Sequence 2598, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
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PRIOR
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ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2000-05-26
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Yamamoto, Robert T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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d, Judith W.
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52.9%;

 Mismatches

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US-10-156-761-1
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APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIKA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
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APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
TCHTKAWA, JUN
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 2598
LENGTH: 498
                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1
                                                                                                                                                                                                                        Query Match
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Streptomyces avermitilis
PEATURE:
NAME/KEY: misc feature
LOCATION: (4187715)
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LOCATION: (1)..(498)
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                                   3210073 TACGTGGTGATGACCGCGGGCTCGTTCGACATCCTCGCCGAGATCGTCTGCGAGGACGAC 3210132
                                                                                                               3210013
                                                                                                                                                                                                       Match 11.2%;
Local Similarity 51.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 CATGTCGAGGGGACCTCGACCCGGTCGCGGACGCGCTGACCGCCATGTCGGAAGTCGAG
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                                                                      71 GACATTGCGATGAAAGATGGGACCGCYGACGTCCTTGGCGGGGGGGGGAGCGCGAGAACCAA 130
                                                                                                                                              11 CGYTTSGCTCGGTGCATGCAGAAGGACGGGWTGAAGGCGGACGGGATTGACGACGACGAC 70
                                                                                                                                                                                     6;
CATGTCGAGGGGGACCTCGACCCGGTCGCGGACGCGCTGACCGCCATGTCGGAAGTCGAG 3210072
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Pred. No. 0.00:
3; Mismatches
                                                                                                                                                                                                       Score 41.6; DB 14; Pred. No. 0.029;
                                                                                                                                                                                       Mismatches
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Best Local Similarity
Thes 71; Conserve
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                                                                                                                                                                                                                                                                                  APPLICANT: MEDRANO, JUAN
APPLICANT: HEADFORD, ERIC
APPLICANT: HEADFORD, ERIC
FALENT: HORVAT, SIMON
TITLE OF INVENTION: CLONING OF A HIGH-GROWTH GENE
FILE REFERENCE: 407T-923710US
CURRENT APPLICATION NUMBER: US/09/771,208
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 08/999,477
PRIOR FILING DATE: 1997-12-29
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
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US-09-771-208-20/c
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SEQ ID NO 31
LENGTH: 228
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                                                                                                                                                                                                                                                             SEQ ID NO 20
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CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: PCT/JPD1/00678
PRIOR FILING DATE: 2001-01-31
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PRIOR FILING DATE: 2000-01-31
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OTHER INFORMATION: Parental Oka strain
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ORGANISM: Varicella virus
FEATURE:
NAME/KEY: misc_feature
LOCATION: (123459)..(123478)
                                                                                                                            TYPE: DNA ORGANISM: Mus musculus
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                                                                                                                                                                                                         LENGTH: 659158
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TAKAHASHI, Michiaki
YAMANISHI, Koichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 0.0073;
0; Mismatches 51;
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Search completed: September 15, Job time: 192 secs
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LOCATION: (132580)..(132700)
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LOCATION: (346860)..(346823)
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LOCATION: (390986)..(391005)
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LOCATION: (494715)..(494814)
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LOCATION: (17625)...(170645)
OTHER INFORMATION: n is unidentified
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LOCATION: (183872)..(183891)
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LOCATION: (271829)..(271848)
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## ALIGNMENTS

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Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,	545	533	Nat. Genet. 25 (2), 235-238 (2000)	using Tetraodon nigroviridis DNA sequence	Estimate of human gene number provided by genome-wide analysis	Saurin, W. and Weissenbach, J.	Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,	Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,		Tetradontoidea; Tetraodontidae; Tetraodon.	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Tetraodon nigroviridis	Tetraodon nigroviridis	GSS; genome survey sequence.	AL223102.1 GI:7881921	102	ace.	204G08 of library G from Tetraodon nigroviridis, genomic survey	Tetraodon nigroviridis genome survey sequence T7 end of clone	151 879 bp DNA linear GSS 01-SEP-2000		

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage
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                                                                                                                                                                                                                Anderson,O.D., Butler,E., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Gustafson,J.P., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Ross,K., Seaton,C.L. and Tong,J.C. The structure and function of the expressed portion of the wheat genomes - Anther cDNA library from rye
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WHE1257_G04_N07ZS Secale cereale anther cDNA library CDNA Clone WHE1257_G04_N07, mRNA sequence.

BE494661
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This sequence is a single read and was generated as
                                                                                                           Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                               Secale cereale (rye)
Secale cereale
Secale cereale
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea;
Triticeae; Secale.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon. Location/Qualifiers
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Email: oandersn@pw.usda.gov
Sequence have been trimmed
quality sequence with phred
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE494661
                                                                                                                                                                                              Unpublished
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                                                                     Fax: 5105595818
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  s have been trimmed to remove vector sequence with phred score less than
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/clone_lib="G"
/note="Genoscope sequence ID : C0AG204BD04LP1~end :
/note="Genoscope sequence ID : C0AG204BD04LP1~end :
/note="Genoscope sequence ID : C0AG204BD04LP1~end :
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/mol type="genomic DNA"
/db xref="texoon:99883"
/clone="204G08"
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Pred. No. 0.095;
4; Mismatches
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
enermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
Sequence have been trimmed to remove vector quality sequence with phred score less than Seq primer: Stratagene SK primer.
                                                                                                                      US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                            Spermatophyta; Magnoliophyta;
Triticeae; Secale.
1 (bases 1 to 490)
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                                                               Email: oandersn@pw.usda.gov
                                                                                                                                                                                     Contact: Olin Anderson
                                                                                                                                                                                                        Unpublished
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//lab_bost="E. coli SQLR"
//clone_lib="Secale cereale anther cDNA library"
//clone_lib="Secale cereale anther cDNA library"
//clone_lib="Secale cereale anther cDNA library"
//note="Wector: Lambda Uni-ZAP XR, excised phagemid;
Site_l: EcoRI; Site_2: XhoI; Plants were grown in the
greenhouse. Anthers were harvested and pooled from early
meiosis to late meiosis. The tissue, total RNA, and
poly(A) RNA were prepared (Butler, Ross and Gustafson) at
University of Missouri, Columbia. A cDNA library was
made, and the CDNA clones were in vivo excised to give
pBluescript phagemids in the TJ Close lab (Choi, Close,
Fenton) at the University of California, Riverside.
Pensmid DNA preparations and DNA sequencing were performed
in the OD Anderson lab (all other authors)."
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Location/Qualifiers
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/clone="WHE1257_G04_N07"
/tissue_type="Anther"
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/cultivar="Blanco"
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AUTHORS
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quality sequence with phred score
Seq primer: Stratagene SK primer.
Location/Qualifiers
                                                                                                                                                                                                                                                     Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 557)
Anderson,O.D., Butler,E., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Gustafson,J.P., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Ross,K., Seaton,C.L. and Tong,J.C.
The structure and function of the expressed portion of the wheat genomes - Anther cDNA library from rye
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BF145396.1 GI:11026827
EST.
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                                                                                                                                                                                                                                                                                                                                                Unpublished
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                                                                                              Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector
                                                                                                                                                                                            800 Buchanan Street, Albany,
Tel: 5105595773
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/clone="WHE1255_CO7_E13"
/tissue_type="Anther"
/dev_stage="Adult plant before anthesis"
/lab_host="E. coli SOLR"
/clone_lib="Secale_cereale_anther_CDNA_library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Secale.
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60.3%;
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Pred. No. 0.17;
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                                                               less than
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JOURNAL COMMENT
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BF621513/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BF621513 816 bp mRNA linear EST 18-OCT-2001
HVSMEa0011D21f Hordeum vulgare seedling shoot EST library
HVcDNA0001 (Cold stress) Hordeum vulgare subsp. vulgare cDNA clone
                                                                                                                                                                      Unpublished
On Dec 18, 2000 this sequence version replaced gi:13083392.
Contact: Wing RA
                                                                                                                                                                                                                                                       1 (bases 1 to 816)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Oates,R., Choi,D.W., Fenton,R.D. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex cold-stressed seedling shoot cDNA
                                                                                                                                                                                                                                                                                                                                                                                                              Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
                                                               Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                    Clemson University
                                                                                                                                                 Clemson University Genomics Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HVSMEa0011D21f, mRNA sequence.
Seq primer: AATTAACCCTCACTAAAGGG
                    Total hq bases = 552
                                        Email: rwing@clemson.edu
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/lab host="E. coli SOLR"
/clone lib="Secale cereale anther cDNA library"
/clone lib="Secale cereale anther cDNA library"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XNoI; Plants were grown in the
greenhouse. Anthers were harvested and pooled from early
meiosis to late meiosis. The tissue, total RNA, and
poly(A) RNA were prepared (Butler, Ross and Gustafson) at
University of Missouri, Columbia A cDNA library was
made, and the CONA clones were in vivo excised to give
pBluescript phagemids in the TJ Close lab (Choi, Close,
Fenton) at the University of California, Riverside.
Plasmid DNA preparations and DNA sequencing were performed
in the OD Anderson lab (all others)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="WHE1841-1844_B21_B21"
/tissue_type="Anther"
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/cultivar="Blanco"
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Pred. No. 0.17
1; Mismatches
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JOURNAL COMMENT
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TITLE
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ORGANISM
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                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 464)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                 BE799902.1 GI:10221100
EST.
                                                                                                                                                                                                                                                                                                                                     601588045F1 NIH_MGC_7 Homo
                                                   Contact: Robert Strausberg, Ph.D
                                                                          Unpublished
                                                                                                                                                                                                                                                                                                              mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                           BE799902
                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                           Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              // Note="Vector: lambdaZAP; Site 1: EcoR1; Site_2: Xho1; // Note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; // Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystaatin and cefcotaxime in covered crystallization dishes. Five-day old seedlings were incubated at 5oC for 2 days. Shoots were then harvested, total RNA was prepared, poly(A) RNA was gurified, one primary unamplified cDNA library was made, and 600000 pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main ). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and
Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
http://wheat.pw.usda.gov/gpages/bgn/31/cover.html)"
a 270 c 271 g 134 t
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HVcDNA0001 (Cold stress)"
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| lab_host="TJC121"
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                           464 bp
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131 GACGACGAGGACGACGTCTACG 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        wkm2n.pk004.g21 wkm2n Triticum
5' end, mRNA sequence.
CA719534
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High quality sequence stop: 215.
Location/Qualifiers
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Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 485)
Tingey, S.V., Powell, W., Wolters, P.,
Miao, G., Caraher, N. and Hanafey, M.K.
DuPont Wheat cDNA Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Tritice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA719534.1 GI:25441327
                                Seq primer: M13.
                                                                                                                                                                                                                                                                                                           Crop Genetics
                                                                                                                                                                                                                                                                                                                                                          Contact: Scott V. Tingey
                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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                                                                                                                                                                   I. DuPont de Nemours and Company Innovation Way, P.O. Box 6104, New el: 302-631-2602
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/clone lib="NIH MGC 7"
/clone lib="NIH MGC 7"
/cotone lib="NIH MGC 7"
/cotone lib="Coton lung; Vector: pOTB7; Site 1: XhoI; Site 2:
/cotoned into EcoRI/XhoI sites using the following 5;
cloned into EcoRI/XhoI sites using the following 5;
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
06 a 125 c 145 g 88 t
                                                                               Scott.V.Tingey@USA.dupont.com
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/tissue_type="small cell carcinoma"
/cell_line="MGC3"
Location/Qualifiers
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/db_xref="taxon:9606"
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wkm2n.pk004.g21
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                  Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol., (2002) In press
Contact: Chris K. Raymond
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                                                                                                                                                                                                                                                             University of Washington
Box 352145, Seattle, WA 98105-2145,
                                                                                                                                                                                                                                                                                        Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genomic survey sequence.
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                                                                                                                                                                                                           shot
                                                                                                                                                                                                                   craymond@u.washington.edu
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/clone="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
XhoI; Wheat (Triticum aestivum L.) kernel malted 175 hours
at 4 C, normalized"
a 147 c 172 g 65 t 2 others
                                                      library."
a 345 c
                                                                              /clone="msh2_4267"
/clone_lib="msh"
/note="Environmental
                                                                                                                        /strain="MSH"
/db_xref="taxon:287"
                                                                                                                                                                organism="Pseudomonas aeruginosa"
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/tissue_type="kernel"
/lab_host="DH10B"
                                                                                                                                                                                           ocation/Qualifiers
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/cultivar="Spring wheat"
/db_xref="taxon:4565"
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12.0%;
50.5%;
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192 CCTCCGCATTGCTGAT 207
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CD056167
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Tel: 0049 (0)39482-5660
Fax: 0049 (0)39482-5595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CD056167 444 bp mRNA linear EST 05-JH H011G01S HO Hordeum vulgare cDNA clone H011G01 5-PRIME, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barley ESTs from pathogen-attacked leaf epidermis Unpublished
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Zierold, U. and Schweizer, P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Patrick Schweizer
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     89
                 /clone lib="HO"

/clone lib="HO"

/note="Vector: pBluescript SX+; Site_1: EcoRI (5'-end of cDNA); Site_2: XhoI (3'-end of cDNA); Approximately 5 % of the clones correspond to cDNA from the fungi B. graminis hordei and tritici, respectively. Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, Sall, Pstl). NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable. Average insert size is 1.2 kb"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vulgare
                                                                                                                                                                                                                                                                                                                     inoculation with Blumeria graminis"
/dev_stage="7 d after germination"
/lab_host="XL10-Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/cultivar="Ingrid BC mlo-5"
/db_xref="GABI:707130"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          tissue_type="leaf_epidermis, 6 h and
                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                         clone="HO11G01"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 CGGGATTGACGACGACGACGACGATGCGATGAAAGATGGGACCGCYGACGTCCTTGGCGG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8884 Fax: 516 367 8874
                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plate: hgll row: g colum
Seg primer: -21M13UnivRev
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                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 449
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mccombie@cshl.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: W. Richard McCombie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; seterids; lamiids; Gentianales; Rubiaceae; Rubioideae; Spermacocea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hg11g07.g1 Hedyotis centranthoides flower - Stage 2 centranthoides cDNA clone hg11g07, mRNA sequence.
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   AGCTGGTCGTTGATGACGTTGAAGATGAAGACGATGACGACGACGACGACGACGACGACAACG
                       TGGÁGGÁGGÁATTTAGGGCGGCTGÁCGGAGTTGAAGGCAAGGAGGAGTTTGGGGAAGGAAG
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                                                                                                                                                                                                       /note="Organ: flower; Vector: pBK-CMV; Site_1: XhoI; Site_2: Eco RI; Date: Completed 12/18/01. Sübmitted to CSHL 12/21/01 Library: Stratagene ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts. Sample: collected on the island of Hawaii, Hawaii, NGG herbarium voucher TM2563" a 60 c 157 g 97 t
                                                                                                                                                                                                                                                                                                                                                                            /organism="Hedyotis centranthoides"
/mol_type="mRNA"
/db_xref="taxon:219666"
                                                                                                                                                                                                                                                                                                                                (clone="hg11g07"
'dev_stage "pre-anthesis; Stage 2"
'clone_lib="Hedyotis centranthoides flower -
                                                                                                                                               11.8%;
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                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: stein@ipk-gatersleben.de
Insert Length: 470 Std Error:
Plate: 5 row: D column: 13
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Tel: 039482-5522
Fax: 039482-5595
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Institute of Plant Genetics and Crop Plant |
Corrensstr. 3, 06466, Gatersleben, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Stein Nils
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barley ESTs from germinating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang, H., Potokina, E., Michalek, W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HU05D13r HU Hordeum vulgare subsp.
                       GGCGGAGCGCGAGAACCAAGACGACGAGGACGAGGACGTCTACGCGCGCATCC
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CGGGATTGACGACGACGACATTGCGATGAAAGATGGGACCGCYGACGTCCTTGGCGG 111
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                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="GABI:264272"
/db_xref="taxon:112509"
                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/cultivar="barke"
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                                                                                                                                                                                                                                                                                                                                                                tissue_type="germinating seeds"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Hordeum vulgare subsp. vulgare"
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                                                                                                                                        Length 470;
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cDNA clone HU05D13
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BQ464793
BQ464793.1 GI:21272575
EST.
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                                                                                                                    CA029558

CA029558

HZ65J0Ir HZ Hordeum vulgare subsp.
5-PRIME, mRNA sequence.
CA029558

CA029558.1 GI:24307522
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Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Institute of Plant Genetics and Crop Plant
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: stein@ipk-gatersleben.de
Insert Length: 514 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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//Glone_lib="HU"
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/dev_stage="germinating seeds, 1
/lab_host="XL10-Gold"
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/clone="HU01I14"
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Pred. No. 1.2;
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
1 (bases 1 to 531)
Zhang, H., Weschke, W., Michalek, W., Stein, N. and Graner, A.
EST sequencing and analysis in barley (2002)
Unpublished
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Contact: Stein Nils
Molecular Markers Group, Department G
Institute of Plant Genetics and Crop
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1 (bases 1 to 530)
Radchuk, V., Zhang, H., Weschke, W., Potokina, E. and Wobus, U.
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Contact: Stein Nils
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//dev_stage="0-7 DAP (days after pollination)"
//lab_host="XI10-Gold"
//clone_lib="HZ"
//clone_lib="HZ"
//clone_lib="HZ"
//clone_lib="HZ"
//note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of CDNA); Site 2: XhoI (3'-end of cDNA); pericarp 0-7
DAP(days after pollination). Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI asded pter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PatI). NOTE: Also due to the cloning system used Blue/white selection for recombinate is not 100% reliable.Average insert size is 900 bp"
78 a 180 c 201 g 70 t l others
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                                       Department Genbank
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REFERENCE
AUTHORS
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ORGANISM
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BU771970
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VERSION
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ORIGIN
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JOURNAL
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Best Local Similarity
Matches 69; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 CGGGATTGACGACGACGACGACGATTGCGATGAAAGATGGGACCGCCCGGCGGTCCTTGGCGG 111
                                                                                                                   Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                        1 (bases 1 to 923)
Hu,W., Yan,Q., Shen,D., Liu,F., Xu,X., Zhu,Z., Zhang,X., Wang,J.,
Sun,J., Xu,X., Wang,Z., Zeng,L., Rong,Y., Wu,X., Qu,J., Xu,Z.,
Huang,J., Ma,Y., Wang,S., Wang,Z., Xue,C., Feng,Z., Chen,Z. and Han
                                                                                                                                                                                                                                                                                                                                                                                            Schistosoma japonicum
Schistosoma japonicum
Schistosoma japonicum
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
                                                                                                                                                                                                                                                     Expressed sequence tags from eggs of Schistosoma japonicum Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BU771970
SJEELA02 SJE Schistosoma
                                                                               Email: hanzg@chgc.sh.cn.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BU771970
BU771970.1 GI:28339286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: stein@ipk-gatersleben.de
Insert Length: 531 Std Error: 0.00
Plate: 12 row: A column: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCGGAGCGCGAGAACCAAGACGACGACGACGACGTCTACGCGCGCATCC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGTGCTCCACGACGTCGCCGCCCAGGCGCGGGTCGACGGCTCCGGTGACCGTGCCGGCGC 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev stage="female inflorescences (approx. 3 mm in size)"
/lab_host="XL10-Gold"
/clone_lbb="HI"
/clone_lbb="HI"
/note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of cDNA); Site_2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI Site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI,PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinate is not 100% reliable."
/organism="Schistosoma
/mol_type="mRNA"
/db_xref="taxon:6182"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "mol_type="mRNA"
'cultivar="barke"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Hordeum vulgare subsp. vulgare"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        xref="taxon:112509"
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                                       japonicum"
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ORIGIN
                                                                                                            Matches
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Best Local
130 ACGACGACGACG 141
                 144 AGGACGTCTACG 155
                                                  10
                                  24 GCATGCAGAAGGACGGGWTGAAGGCGGACGGACGACGACGACGACGATGA 83
                                                                                                            75;
                                                                                                          h 11.8%;
Similarity 56.8%;
75; Conservative
                                                                      303 a
                                                                                                                                                     /tissue_type="Whole e
/dev_stage="egg"
/lab_host="rabbits"
/clone_lib="SJE"
a 405 c 179 g
                                                                                                                                                      /clone_lib:
                                                                                                          Score 43.8; D
Pred. No. 1.3;
2; Mismatches
                                                                                                                                                                                           egg"
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4
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                                                                                                                             DB 13;
                                                                                                           55;
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                                                                       69
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Search co completed: September 15, 2003, 00:33:36 ne : 1971 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
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371
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/cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:*
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/cgn2_6/ptodata/
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|: /cgn2_6/ptodata/2/pna/
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Copyright (c) 1993 - 2003 Compugen Ltd.
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	<pre>cgn2_6/ptodata/2/pna/US6046_COMB.seq cgn2_6/ptodata/2/pna/US6047_COMB.seq</pre>	m2_6/ptodata/2/pna/US6044_COMB.se gn2_6/ptodata/2/pna/US6045_COMB.s	gn2_6/ptodata/2/pna/US6043_COMB.se	gn2_6/ptodata/2/pna/US6041_COMB.seq	ata/2/pna/US6040_COMB.se	gn2_6/ptodata/2/pna/US6038_COMB.seq	ata/2/pna/US6037 COMB.seq	gn2_6/ptodata/2/pna/US6035_COMB.seq	gn2_6/ptodata/2/pna/US6034_COMB.seq	/cgn2 6/ptodata/2/pna/US6033 COMB.seq:*	gn2_6/ptodata/2/pna/US6031_COMB.seq	gn2_6/ptodata/2/pna/US6030_COMB.seq	ata/2/pna/US602	gn2_6/ptodata/2/pna/US6027_COMB.seq	gn2_6/ptodata/2/pna/US6026_COMB.seq	ata/2/pna/US6025_COMB	gn2_6/ptodata/2/pna/US6023B_COMB.se	gn2_6/ptodata/2/pna/US6023A_COMB.se	gn2_6/ptodata/2/pna/US6022_COMB.seq	2_6/ptodata/2/pna/US6020_COMB.se	gn2_6/ptodata/2/pna/US6019_COMB.seq	gn2_6/ptodata/2/pna/US6018_COMB.seq	n2 6/ptodata/2/pna/US6017 COMB.seq	gn2_6/ptodata/2/pna/US6015_COMB.se	gn2_6/ptodata/2/pna/US6014_COMB.seq	gn2 6/ptodata/2/pna/US6013 C	z_6/ptodata/2/pna/US6012_COMB.seq	gn2_6/ptodata/2/pna/US6010_COMB.seq	gn2_6/ptodata/2/pna/US6009_COMB.seq	ata/2/pna/US600	gn2_6/ptodata/2/pna/US6006_COMB.se	gn2_6/ptodata/2/pna/US6005_COMB.seq	/cgn2_6/ptodata/2/pna/US6004_COMB.seq:*	gn2_6/ptodata/2/pna/US6002_COMB.seq	gn2_6/ptodata/2/pna/US6001_COMB.s	gn2_6/ptodata/2/pna/IIS6000_COMB_seq	2_6/ptodata/2/pna/US104A_COMB.seq 2_6/ptodata/2/pna/US104A_COMB.seq	gn2_6/ptodata/2/pna/US103B_COMB.se	/cgnz_6/ptodata/z/pna/US103A_COMB.seq:*	gn2_6/ptodata/2/pna/US102A_COMB.seq	/ptodata/2/pna/US101B_COM	gn2_6/ptodata/2/pna/US100B_COMB.seq	gn2_6/ptodata/2/pna/US100A_COMB.se
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

00 122	Result
369 366.6 50.2	Score
99.5 98.8 13.5 12.7	Query  Match Length DB ID
371 372 1931 597	Length
44 44 44	DB
369 99.5 371 35 US-09-849-729-1 366.6 98.8 372 35 US-09-849-729-2 50.2 13.5 1931 18 US-09-250-359-2 47 12.7 597 44 US-10-020-338-1346	SUMMARIES
Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1346, Ap	cri

Matches

371;

Conservative

100.0%; ++

Pred. No. 9e-81; ); Mismatches 0;

Indels

0,

Gaps

0;

1 GATCMGGAAACGYTTSGCTCGGTGCATGCAGAAGGACGGGWTGAAGGCGGACGGGATTGA

GATCMGGAAACGYTTSGCTCGGTGCATGCAGAAGGACGGGWTGAAGGCGGACGGGATTGA

60 60 Best Local Similarity

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CURRENT APPLICATION NUMBER: US/09/849,729
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/202271
PRIOR FILING DATE: 2000-05-05
NUMBER: OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 371
                        ; TYPE: DNA
; ORGANISM: Sentinel Virus
US-09-849-729-1
                                                                                                                                                                                                                                                                                                                                      RESULT 1
US-09-849-729-1
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                                                                                                                                                                                                                                                     Sequence 1, Application US/09849729
GENERAL INFORMATION:
APPLICANT: Liu, Jen-Kuei
APPLICANT: Lewis, Samantha
APPLICANT: Batz, Hans-Georg
APPLICANT: Ramaswamy, Latha
Query Match
                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                         APPLICANT: Chen, Benjamin
TITLE OF INVENTION: Sentinel Virus II
FILE REFERENCE: RDID 0070
                                                                                                                                                                                                                  APPLICANT:
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0 0 0 0
                                                                                                                                                                                                               Ramaswamy, Latha
Bohenzky, Roy
Lin, Yu-Huei
Montiel, Janine
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WS-09-654-617-444082
US-09-654-617-439911
WS-09-654-617-439911
US-09-654-617-439911
US-09-654-617-439911
US-09-654-617-4755
WS-10-626-717-7755
US-10-626-717-778
WS-10-626-717-778
WS-10-626-713-678
WS-09-702-134-6722
WS-10-366-683-9465
WS-10-366-683-9465
WS-10-366-683-9411
WS-10-366-83-9411
WS-10-366-83-9411
WS-10-366-83-9411
WS-10-366-83-9411
WS-10-366-83-9411
WS-10-366-83-9411
WS-10-366-83-9411
 Score 369;
  DB
 Length 371;
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Sequence 1,
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17907,
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7755, Ap
439911,
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45473, A
41549, Ap
6722, Ap
749830, A
74988, Ap
727, Ap
93465, Ap
9337, Ap
9337, Ap
9311, Ap
9411, Ap
9411, Ap
9411, Ap
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CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/202271
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
                                                                                                Best Local
Matches 36
                                                                                                                                                                 IENGTH: 372

TYPE: DNA
ORGANISM: Sentinel Virus II
FEATURE:
FEATURE:
NAME/KEY: misc feature
LOCATION: (372).(372)
OTHER INFORMATION: unknown: c:
OTHER INFORMATION: in this po
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                                                                                                                          Query Match
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APPLICANT: Lin, Yu-Huei
APPLICANT: Montiel, Jannine
APPLICANT: Chen, Benjamin
TITLE OF INVENTION: Sentinel Virus
FILE REFERENCE: RDID 0070
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Liu, Jen-Kuei
APPLICANT: Lewis, Saman
APPLICANT: Batz, Hans-G
APPLICANT: Ramaswamy, L
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                                                                                                              Similarity
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Bohenzky, Roy
Lin, Yu-Huei
Montiel, Janine
GATCMGGAAACGYTTWGCTCGGTGCATGCAGAAGGACGGGSTGAAGGCGGACGGGATTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lewis, Samantha
Batz, Hans-Georg
                                                                                                98.8%; Score 366.6; DB 35; llarity 99.5%; Pred. No. 3.5e-80; Conservative 0; Mismatches 2;
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; SEQ ID NO 2
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: EBNA
- US-09-250-359-2
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US~10-020-338-1346
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           Sequence 1346, Application US/10020338
GENERAL INFORMATION:
APPLICANT: Andersen, Scott E.
APPLICANT: Urban, Martin
TITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(52272)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09250359
GENERAL INFORMATION:
APPLICANT: Horlick, Robert A.
APPLICANT: Damaj, Bassam B.
APPLICANT: Commaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REPERENCE: 0867/1D903US1
CURRENT APPLICATION NUMBER: US/09/250,359
CURRENT FILING DATE: 1999-02-12
                                                                                                                                                                                                                                                                                                                                                     Matches 79;
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EARLIER FILING DATE: 198-08-08
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 3.0
CURRENT APPLICATION NUMBER: US/10/020,338
                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                  Score 50.2; DB Pred. No. 0.056; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             DB 18;
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                                          Other Molecules Associated
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US-09-654-617-444082; Sequence 444082; App; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Triticum aestivum ; OTHER INFORMATION: Clone ID: LIB103-056-Q1-E1-B1 US-09-540-234-4340
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SEQ ID NO 4340
LENGTH: 373
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GENERAL INFORMATION:
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SEQ ID NO 1346
LENGTH: 597
TYPE: DNA
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Best Local (
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Best Local Similarity
            APPLICANT: KO
APPLICANT: Liu, Ji
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                           Matches
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APPLICANT: Masucci, James D
TITLE OF INVENTION: Nu
TITLE OF INVENTION: plants
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CURRENT APPLICATION NUMBER: US/09/540,234
CURRENT FILING DATE: 2000-04-03
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PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2000-12-14
 FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE: OTHER INFORMATION: Clone ID: LIB3833-014-Q1-K6-H10
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                                                                      Application US/09654617
                          Jingdong
                                          Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conner, Timothy W.
Annotated
38-21(15097)D
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                                                                                                                                                                                                                                                                                                                                       Score 45.4; DB
Pred. No. 0.72;
                                                                                                                                                                                                                                                                                                                           Mismatches
               Plant Genes
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                                                                                                                                                                                                                                                                                                                                                       DB 24;
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CURRENT APPLICATION NUMBER: US/09/684,016
CURRENT FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 09/654,617
PRIOR PLICATION NUMBER: US 09/654,617
PRIOR PLICATION NUMBER: US 09/654,617
PRIOR PLICATION NUMBER: US 09/654,617
PRIOR FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 463173
SEQ ID NO 444082
LENGTH: 373
TYPE: No. 373
US-60-128-437-4849

Sequence 4849, Application US/60128437

GENERAL INFORMATION:

APPLICANT: Conner, Timothy W.

APPLICANT: MASUCCI, James D.

TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Plants

FILE REFERENCE: 38-2115725)A

CURRENT APPLICATION NUMBER: US/60/128,437

CURRENT FILING DATE: 1999-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; CURRENT APPLICATION NUMBER: US/09/654,617; CURRENT FILLING DATE: 2000-09-05; NUMBER OF SEQ ID NOS: 463173; SEQ ID NO 444082

LENGTH: 373

TYPE: DNA

ORGANISM: Triticum aestivum
US-09-654-617-444082
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Matches
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Best Local
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79; Conserv
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nilarity 57.7%;
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Pred. No. 0.72;
1; Mismatches 57;
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                                                          and Other Molecules Associated with
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US-09-790-399-7
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                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
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APPLICANT: Smith, Jonathan D.
APPLICANT: Smith, Jonathan D.
TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Traifill of Invention: Systematic Polypeptide Evolution by Reverse Traifill of Reference: NEXO2/C1-CON2
CURRENT APPLICATION NUMBER: US/09/790,399
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 07/197,649
PRIOR FILING DATE: 1998-11-23
PRIOR APPLICATION NUMBER: 07/829,461
PRIOR APPLICATION NUMBER: 07/829,461
PRIOR APPLICATION NUMBER: 07/739,055
PRIOR APPLICATION NUMBER: 07/561,968
PRIOR FILING DATE: 1990-08-02
NUMBER OF SEQ ID NOS: 26
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SEQ ID NO 4849
LENGTH: 373
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TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Sequ
OTHER INFORMATION: having a 120 repeat of ACG flanked by fi
OTHER INFORMATION: fragments having NcoI restriction sites.
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Similarity 57.8%;
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                                                                                                                                                                                                                                                                            Score 45; DB 33; Pred. No. 0.9;
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SEQ ID NO 7755
LENGTH: 422

TYPE: DNA
ORGANISM: Triticum aestivum
OTHER INFORMATION: Clone ID: uC-tsrow189025e10b1
US-09-594-596-7755
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Best Local S
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Best Local Similarity
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/654,617
CURRENT FILING DATE: 2000-09-05
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CURRENT FILING DATE: 2000-06-15
NUMBER OF SEC IN NO.
                                                                                                                                                                                                                                                                                                                                                                                                           APPEICANT: Liu, Jir
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Byrum, Joseph R.
APPLICANT: De La Pena, Robert C.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: PLANTS
                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Triticum aestivum OTHER INFORMATION: unsure at all n locations
                                                                                                                                                                                                                                                                                                                   LENGTH: 422
                                                                                                                                                                                                      Local Similarity
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                                                                                          CGACGACGACGACATTGCGATGAAAGATGGGACCGCYGACGTCCTTGGCGGGGGCGGAGCG 120
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CGAGGCCGGAGGCGTGGACATCGCCGAGG 223
                           CGAGAACCAAGACGACGAGGACGACG 149
                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                 Score 45; DB 28
Pred. No. 0.91;
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Pred. No. 0.91;
                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                  Length 422
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APPLICANT: Byrum, Joseph R.
APPLICANT: De La Pena, Robert C.
APPLICANT: De La Pena, Robert C.
TITLE OF INVENTION: PLANTS
FILE REFERENCE: 38-21(15878) C
CURRENT APPLICATION NUMBER: US/10/304,123A
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: US 09/594,596
PRIOR APPLICATION NUMBER: US 09/594,596
PRIOR APPLICATION NUMBER: US 09/594,596
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 10952
SEQ ID NO 7755
LENGTH: 422
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US-10-304-123A-7755
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; NAME/KEY: unsure
; LOCATION: (1)..(422)
; OTHER INFORMATION: unsure at all n locations
US-09-684-016-439911
                                                                   ; OTHER INFORMATION: Clone ID: uC-tsrow189025e10b1 US-10-304-123A-7755
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SEQ ID NO 439911
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                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kovalic,
APPLICANT: Liu, Jingdong
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE:
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                                                                                                                   NAME/KEY: unsure
LOCATION: (1)..(422)
OTHER INFORMATION: unsure
                                                                                                     FEATURE:
                                                                                                                                                                         FEATURE:
                                                                                                                                                                                       ORGANISM: Triticum aestivum
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ORGANISM: Triticum
                                                                                                                                                                                                           TYPE: DNA
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                 Local Similarity
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                 12.1%;
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Pred. No. 0.91;
                 Score 45;
Pred. No.
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1 GATCMGGAAACGYTTSGCTCGGTGCATGCAGAAGGACGGGWTGAAGGCGGACGGGATTGA 60

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APPLICANT: Byrum, Joseph R.

APPLICANT: Byrum, Joseph R.

APPLICANT: De La Pena, Robert C.

APPLICANT: DE LA Pena, Robert C.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH TITLE OF INVENTION: PLANTS

FILE REFERENCE: 38-21(15878)D

CURRENT APPLICATION NUMBER: US/10/626,717

CURRENT FILING DATE: 2003-07-25

PRIOR FILING DATE: 2003-07-25

PRIOR APPLICATION NUMBER: US 10/304,123

PRIOR FILING DATE: 2002-11-26

PRIOR APPLICATION NUMBER: US 09/594,596

PRIOR FILING DATE: 2000-06-15

NUMBER OF SEQ ID NOS: 10952

SEQ ID NO 7755

LENGTH: 422

TYPE: DNA

ORGANISM: Triticum aestivum
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US-10-626-717-7755
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APPLICANT: Andersen, Scott E.
APPLICANT: Hammond-Kosack, Kim
APPLICANT: Masucci, James D.
APPLICANT: Urban, Martin
TITLE OF INVENTION: Nucleic Acid Molecules An
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (51838) B
CURRENT APPLICATION UNMBER: US/09/804,730
CURRENT APPLICATION UNMBER: US/09/804,730
CURRENT APPLICATION UNMBER: US/09/804,730
PRIOR APPLICATION UNMBER: US/09/804,730
PRIOR APPLICATION UNMBER: US/09/804,730
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US-09-804-730-7395
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NAME/KEY: unsure

LOCATION: (1)..(422)

OTHER INFORMATION: unsure at all n locations
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Local Similarity 54.4%;
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ORGANISM: Triticum aestivum
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(561)
OTHER INFORMATION: unsure at a...
OTHER INFORMATION: Clone ID: L.:
US-09-804-730-7395
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Search completed: September 15, 2003, 01:23:00 Job time : 2870 secs
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SEQ ID NO 7395
LENGTH: 561
TYPE: DNA
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Pred. No. 0.94
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LIB3352-008-P1-K1-H2
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Gaps

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Minimum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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   Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being part and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compugen
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/cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
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US-10-425-114A-6704
US-10-425-114A-5254
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US-10-425-114A-32896
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US-10-425-114A-5794
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US-10-425-114A-5896
US-10-425-114A-5896
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134768, A
13768, A
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5274, Ap
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33627, A
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5896, A
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37.4	37.4	37.4	37.4	37.6	37.6	37.6	37.6	38.2			38.2							
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
28931,	20197,	2518, A	2344, A	897, App	22836, 1	25800, 1	17820, 1	26406, 2	33345, 1	5781, Ap	25552, A	32749,	22689,	5775, A	7049, Ap	1166, A	5784, A	34008,

## ALIGNMENTS

US-10-425-114A-21585/c ; Sequence 21585, Application US/10425114A ; GENERAL INFORMATION:

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RESULT 2
US-10-425-114A-13792/c
; Sequence 13792, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
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APPLICANT: Zhou, Yihua
APPLICANT: Schou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Schoen, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5331)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 21585
LENGTH: 1827
TYDE: NNA
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Zea mays
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                                                                                                                                                                                                                         TCCAGCGAGTCGGCGCCGAAGAGGTCGGCCACGAACGCCGCC 457
                                                                                                                                                                                                                                                           AGAACCAAGACGACGAGGACGACGTCTACGCGCGCATCC 164
                                                                                                                                                                                                                                                                                                  TCMGGAAACGYTTSGCTCGGTGCATGCAGAAGGACGGGWTGAAGGCGGACGGGATTGACG
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RESULT 3
US-10-646-664-1
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TITLE OF INVENTION: METHODS OF DIRECTING C-O BOND FOR
TITLE OF INVENTION: POLYKETIDE SYNTHASE SYSTEM
FILE REFERENCE: 054030-0031
CCURRENT APPLICATION NUMBER: US/10/646,664
CCURRENT FILING DATE: 2003-08-22
PRIOR APPLICATION NUMBER: US 60/405,245
PRIOR APPLICATION NUMBER: US 60/405,245
PRIOR FILING DATE: 2002-08-22
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: LIB143-044-G12_FLI US-10-425-114A-13792
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CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 13792
LENGTH: 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Shen, Ben
APPLICANT: Hyung-Jir
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Best Local Similarity
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Streptomyces griseus
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                                                                                                                                                    CGATGAAAGATGGGACCGCYGACGTCCTTGGCGGGGGGGGAGCGAGAACCAAGACGACG
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                                                                                                                                                                                CATGICTITCCCCCCCCTGTTC 15294
                                                            AGGGTGAGGGCGGCAGGCAGCTCGCCGGGTTCCTCGCGGGCCAGAAGTTCATCTAGTCCG
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                          CATTGCTGATCCTGAAGTTC
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Pred. No. 0.086;
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US-60-485-450-67
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APPLICANT: CHANG, Sheng-Yung
APPLICANT: CHANG, Sheng-Yung
TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPA
TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPA
TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001470
CURRENT APPLICATION NUMBER: US/60/485,450
CURRENT FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 47859
SOFTWARE: PSASESEQ for Windows Version 4.0
SEQ ID NO 11874
LENGTH: 100537
TYPE: DNA
ORGANISM: Homo sapiens
US-60-485-450-11874
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GENERAL INFORMATION:
APPLICANT: CHANG, Michele
APPLICANT: CHANG, Sheng-Yung
ITILE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001470
FILE REFERENCE: CL001470
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CURRENT FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 47859
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 67
LENGTH: 3435
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APPLICANT: CARGILL, Michele
APPLICANT: CHANG, Sheng-Yu
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Best Local Similarity
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                                                                                   28 GCAGAAGGACGGGWTGAAGGCGGACGGGATTGACGACGACGACGACATTGCGATGAAAGA 87
                                                                                                                                                                                                                           10.6%;
Similarity 49.8%;
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Conservative
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                                                                                                                                                                                                                           Score 39.4; DB 7;
Pred. No. 0.18;
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                                                                                                                                                                                                                                                                           RESULT 7
US-10-45-114A-34686/c
S-quence 34686, Application US/10425114A
; GENERAL INFORMATION:
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US-10-425-114A-34768/c
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NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 34768

LENGTH: 993
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SEQ ID NO 34686
LENGTH: 1068
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Best Local Similarity
                                    TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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ORGANISM: Zea mays
FEATURE:
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Screen, Steven E
Tabaska, Jack E
Cao, Yongwei
                                                                                                                                                   Zhou, Yihua
Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
Cao, Yongwei
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: 38-21(533i3)B; CURRENT FILIC DATE: 2003-044-28; NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 19765
LENGTH: 864
TYPE: DNA
ORGANISM: Case The Control of the Co
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US-10-425-114A-6704
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                                     RESULT 9
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Best Local Similarity
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Local Similarity 54.1%;
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                                                                                                                                                                                                                                                                                                                                                            TGGGACCGCYGACGTCCTTGGCGGGGGGGGAGCGAGGAACCAAGACGACGAGGACGAGGA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGACGGAGGAGCTGTAGGACTCGACGGAGAGCGACGGCGGCGGCGGCGATGGTGATGC 375
                                                                                                                                                                                                                    CGTCTACGCGCGCAT 162
                                                                                                                                                                                                                                                                                            AGGACG 149
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Pred. No. 0.
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Sequence 6704, Application US/10425114A GENERAL INFORMATION: APPLICANT: Liu, Jingdong

Zhou,

Yihua

APPLICANT: APPLICANT: APPLICANT:

Kovalic, David R Screen, Steven E Tabaska, Jack E Cao, Yongwei

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APPLICANT:

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                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 19745
LENGTH: 965
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 6704
LENGTH: 950
                                                                                                                                                                                             Query Match
Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                   ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                     FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
 597
                            148
                                                           537
                                                                                                                     477
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                                                                                      GCAGAAGGACGGGWTGAAGGCGGACGGGGATTGACGACGACGACGACATTGCGATGAAAGA
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                            CGTCTACGCGCGCAT 162
                                                         GAAGGACGGCGGCGACGAGACGGCGACAAGAAGGACGAGGCCGGCGACAAGGACAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCGGCCGCCAGCCT
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Screen, Steven E
Tabaska, Jack E
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                                                                                                                                                                                 Conservative
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Pred. No. 0.09;
2; Mismatches 60;
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                                                                                                                                                                                                           Length 965;
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RESULT 11

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US-10-425-114A-5274
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SEQ ID NO 5274
LENGTH: 1366
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                                                                                                Matches
                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                  APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
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APPLICANT:
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TYPE: DNA
ORGANISM: Zea mays s
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                             ORGANISM: Zea mays FEATURE:
                                                                                                                                                                                                                                 TYPE: DNA
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                                659 ATCGAGGACGCCATCGACGCCGATCAGCTGGCTGGACGCCAACCAGCTCGCCGAGGCG
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 80 ATGAAAGATGGGACCGCYGACGTCCTTGGCGGGGCGGAGCGCGAGAACCAAGACGACGAG 139
                                                              20 CGGTGCATGCAGAAGGACGGGWTGAAGGCGGACGGACGACGACGACGACGACGACGTTGCG 79
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                                                                                                               Similarity
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Kovalic, David
Screen, Steven
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Screen, Steven
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                                                                                                Conservative
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Pred. No. 0.1;
2; Mismatches
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; OTHER INFORMATION: Clone ID: 700458467_FLI US-10-425-114A-5524
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US-10-425-114A-5525
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Best Local S
Matches 73
                                                                                            NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 5524
LENGTH: 1498
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LENGTH: 1431
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APPLICANT: Liu, Jingdong
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                                                                                                                                                    APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)18
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
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APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: 2003-04-28
RUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua
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ORGANISM: Zea mays
                                 FEATURE:
                                                      ORGANISM: Zea mays
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Similarity 54.1%;
73; Conservative
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            Search completed: September 15, 2003, 01:24:35
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Job time : 76 secs
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated '
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 17354
LENGTH: 1643
TYPE: DNA
ORGANISM: Zea mays
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Best Local Similarity
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, Davi
APPLICANT: Screen, Steve
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Screen, Steven E
Tabaska, Jack E
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54.1%;
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Pred. No. 0.11;
2; Mismatches 60,
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